

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2001, 16:08:57 ; Search time 2886.99 Seconds
(without alignments)
4327.146 Million cell updates/sec

Title: US-08-816-011C-1
Perfect score: 2441
Sequence: 1 acgcgacgcgcgcgagtgta.....atctgattcgtcgctcgag 2441

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_om: *
4: gb_ov: *
5: gb_ph: *
6: gb_pl1: *
7: gb_pl2: *
8: gb_pr1: *
9: gb_pr2: *
10: gb_pr3: *
11: gb_ro: *
12: gb_sy: *
13: gb_un: *
14: em_fun: *
15: em_hum1: *
16: em_hum2: *
17: em_in: *
18: em_om: *
19: em_or: *
20: em_ov: *
21: em_pat: *
22: em_ph: *
23: em_pl: *
24: em_ro: *
25: em_sy: *
26: em_sy: *
27: em_un: *
28: em_vi: *
29: gb_ba3: *
30: gb_in1: *
31: gb_in2: *
32: gb_in3: *
33: gb_pl3: *
34: gb_pr4: *
35: em_ba1: *
36: em_ba2: *
37: em_htg1: *
38: em_htg2: *
39: em_htg3: *
40: em_htg4: *
41: em_htg5: *
42: em_htg6: *
43: em_htg7: *

44: em_htg8: *
45: em_htg9: *
46: em_htg10: *
47: em_hum3: *
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49: em_hum5: *
50: em_hum6: *
51: gb_pr5: *
52: gb_pr6: *
53: gb_pr7: *
54: gb_htg1: *
55: gb_htg2: *
56: gb_htg3: *
57: gb_htg4: *
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72: gb_htg19: *
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74: gb_htg21: *
75: gb_htg22: *
76: gb_htg23: *
77: gb_sts1: *
78: gb_sts2: *
79: gb_vil: *
80: gb_vil2: *
81: gb_pat1: *
82: gb_pat2: *
83: em_htg0: *
84: gb_htg24: *
85: gb_pr8: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2441	100.0	2441	81	126670 Sequence 1
2	2371.8	97.2	3568	32	DM055321 U55321 Drosophila
3	1282.2	52.5	21163	58	AC013909 Drosophila
C	4	1282.2	52.5	314087	30 AE003484 AE003484 Drosophila
	5	165.2	6.8	33463	57 AC012766 Drosophila
6	57.8	2.4	1887	11	AF006824 Mus muscu
7	56.2	2.3	897	11	AF022821 Mus muscu
8	56.2	2.3	1888	11	AB008537 Mus muscu
9	56.2	2.3	2009	11	AB013345 Mus muscu
10	55.6	2.3	321	51	AX003049 Sequence
11	55.6	2.3	1236	10	AF129399 Homo sapi
12	55.6	2.3	1246	51	AX003047 Sequence
13	55.6	2.3	1252	34	AF171068 Homo sapi
14	55.6	2.3	2106	10	AF004711 Homo sapi
15	54.6	2.2	2077	11	AF031384 Rattus no
16	54.6	2.2	2772	34	AF247042 Homo sapi
17	53.4	2.2	2590	10	AF006823 Homo sapi
18	53.2	2.2	2730	34	AF279890 Homo sapi
19	52.4	2.1	1794	11	AX018705 Sequence
20	52.4	2.1	1795	11	AF056492 Mus muscu
21	52.2	2.1	1993	11	AX018706 Sequence

22	52.2	2.1	1994	11	AX003051	Sequence	AX003051
23	52.2	2.1	3580	11	MM073488	Mus musculus	U73488
24	51.6	2.1	1854	11	AF119695	Rattus no	AF119695
25	49	2.0	1017	34	AF281302	Homo sapi	AF281302
26	49	2.0	2180	51	AX020359	Sequence	AX020359
27	49	2.0	2180	81	A94721	Sequence	A94721
28	49	2.0	2649	10	AF134149	Homo sapi	AF134149
29	49	2.0	2671	10	AF117708	Homo sapi	AF117708
30	48.6	2.0	1219	30	AB036345	Drosophill	AB036345
31	48.6	2.0	37888	59	AC017571	Drosophill	AC017571
32	48.6	2.0	71457	30	AC005655	Drosophill	AC005655
33	48.6	2.0	232156	30	AE003819	Drosophill	AE003819
34	47.6	2.0	47518	60	AC020452	Drosophill	AC020452
35	47.6	2.0	76743	30	AC005473	Drosophill	AC005473
36	47.6	2.0	79114	54	AC005475	Drosophill	AC005475
37	47.6	2.0	168301	37	AC007302	Drosophill	AC007302
38	47.6	2.0	263411	30	AE003838	Drosophill	AE003838
39	47.4	1.9	2332	34	AK022344	Homo sapi	AK022344
40	46.8	1.9	1125	34	AF212829	Homo sapi	AF212829
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42	46.8	1.9	1158	11	AF212827	Cavia por	AF212827
43	45.4	1.9	1224	53	HSU09065	Human pota	U90065
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45	45.4	1.9	1882	53	HSU033632	Human two P	U33632

ALIGNMENTS									
RESULT	1	I26670	2441 bp	DNA	PAT	07-OCT-1996			
LOCUS	Sequence 1 from patent US 5559026.								
DEFINITION	I26670								
ACCESSION	I26670								
VERSION	I26670.1 GI:1606540								
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 2441)								
AUTHORS	Price,L.A. and Pausch,M.H.								
TITLE	Genes encoding a novel family of potassium channels								
JOURNAL	Patent: US 5559026-A 1 24-SEP-1996;								
FEATURES	Location/Qualifiers								
source	1..2441								
BASE COUNT	555 a 702 c 665 g 519 t								
ORIGIN									
Query Match 100.0%; Score 2441; DB 81; Length 2441;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	1	ACGGGATCGCGCGAGGTATATTTTTTTTACCTCAGTCTCAGTGTTCGGGATCT	60						
QY	61	ctttaaagaaaaaaataaagtcacaaactacacacacacagcgaagcgcaag	120						
Db	61	CTTTAAAGAAAAAATAAAGTCAAACCTACAAACCCACACAGCGAAGCGCAAG	120						
QY	121	caacggttcctgcgagtgatttttttttttttttttttttttttttttttttttttt	180						
Db	121	CACCGGTTCCTCGAGGTGTTATTTTTTTTCAACAAATTTTTCAGTCTCAGTGTTC	180						
QY	181	ccgtcagcagtcgcgcgaatcgatggtctcgtcgtcattcttctacattctcactcg	240						
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QY	241	atgttcgggcgcgaactctattaccattatgacacgcgcgcgcgcgcgcgcgcgcgc	300						
Db	241	ATGTCGGGCGCGCAATCTATTACCATATTAGCAGCGCGCGGAGAGAGATATCGCGCC	300						

QY	301	gaacagcgcaagcgcaaatgtgaatcaatcaacgaatatctgtctggaggagctgggcgacaag	360
Db	301	GAACAGCGCAAGCGCAAAATTGCAATCAACGAATATCTGCTGGAGAGAGCTGGCGCACAAG	360
QY	361	aatacgcacacacaggatagattcttcaacggatctcgggattaactgtgacaaacgggtt	420
Db	361	AATACGACACACAGGATGAGATTCTTCAACGGATCTCGGATTACTGTGTCACAAACCGGTT	420
QY	421	acattgcgcgcgacatatgatagatagccttacacgtggagaccttctaccatgccttcttc	480
Db	421	ACATTGCCGCGACATATGATACGCCCTACAGTGGACCTTACCATGCCCTTCTTTC	480
QY	481	ttcgcttcaacctgttgcctcaacggtgggatagggaatatatcgcgaacacaccttcgc	540
Db	481	TTCGGCTTCAACGTTTGTCTCACGGTGGGATATGGGATATATCGCCACACACCTTCGCC	540
QY	541	ggacggatgatcatgcgtatttcggtgattggcatcccccggtcaaatggtatctctctt	600
Db	541	GGACGGATGATCATGATCGGTATTTCGGTATTGGCATCCCGTCAATGGTATCTCTCTTT	600
QY	601	gccggcctcggcgaatactttggacgtacgttttgaagcgatctacagacgctacaaaaag	660
Db	601	GCCGGCCTCGCGGAATATCTTTGGACGTACGTTTGAAGCGATCTACAGACGCTTACAAAAA	660
QY	661	tacaagatgtccacgggatgcactatgtccgcgcgcagctgggattgatcaccacgggtg	720
Db	661	TACAGATGTCACGGGATATGCATATGTCCGCCGCGAGCTGGGATGATCATCACACGGTG	720
QY	721	gtgattgcccctgattccgggaatagctctcttcctggctgctgcctcgcgtgggtgttcac	780
Db	721	GTGATTGGCTTGAATTCGGGAATAGCTCTCTTCCTGGTGTCTGCCCTGCGTGGGTGTTTAC	780
QY	781	ctaactcgagaactgggocctatcttccactcctcgtctgactacagctatgtgacaccaca	840
Db	781	CTACTTCGAGAACTGGGCCTATCTTCCATCTCGCTGTACTACAGTATGTGACCAACACA	840
QY	841	acaattgattcggtgactatgtgccacatttggagccacacagccacgaagaggttcggc	900
Db	841	ACAATTGGATTGGGTGACTATGTGCCACATTTGGAGCCACACACCCCAAGGATTCGGC	900
QY	901	ggctggctcgtggtctatcacagattttgtgctggtgttctcctcgtcgtgggat	960
Db	901	GGCTGGTTCGTGGTCTATCAGATCTTTCTGATCGTGGTGGTTCATCTTCTCGTGGGATAT	960
QY	961	cttgtgatgatcatgacatttatcaactcggggcctccagagcaagaactggcataacctg	1020
Db	961	CTTGTGATGATCATGCATTTATCCTCGGGGCTTCCAGAGCAAGAAGCTGGCATACCTG	1020
QY	1021	gagcagcagttgtctccaacctgaagccacagatcgcattcgtctggtcgtcacc	1080
Db	1021	GAGCAGCAGTTGTCTTCCAACTGAAGCCACACAGAATCGATCTGTGTGGCGGTACCC	1080
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Db	1081	AAGGATGTGGCTACCTCCGGCGAATGCTCAACGAGCTGTACATCTCTCAAGTGAAGCT	1140
QY	1141	gtgtacacggatgtagatatcgcttacacactgccaacttccaatctcgttccggatctg	1200
Db	1141	GTGTACACCGATGTAGATATCGCTACACACTGCCACCTTCCAATTCGTGTCCGGATCTG	1200
QY	1201	agcattgaccgcgtggagccggtcccaattcccagccggaagagggaattctcgtgtgc	1260
Db	1201	AGCATGTACCCGCTGGAGCCGGCTCCCATTTCCAGCCGGAAGAGGGCAATCTCCGTTGTC	1260
QY	1261	gccgacatggttggcgcacaaaggaggcggtcgtgtgtacacgcgaattcccgatcagat	1320
Db	1261	GCCGACATGTTGGCGCCCAAAAGGAGCGGGCATGGTGTACACGCCAATTCGTACGAT	1320
QY	1321	ctaaccacactggatcgogagaagacattcgagcgcgcggaggcgatccaccacaccacc	1380
Db	1321	CTAACCAACTGGATCGCGAGAAGACATTCCTGAGACGGCGGAGGGGTACCCACAGACC	1380

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QY 1381 gatttgctggccaaggtggttaacacgactgcccacaggtgaagcaccacccgcccggggaacag 1440
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QY 1441 gaagatgcggctctctatggtggtctatcatggtctctccgactccagatccctggtccagc 1500
Db 1441 GAAATGCGGGCTCTCTATGTTGGTGTATCATGGCTTCTCGACTCCAGATCCTGCGCCAGC 1500
QY 1501 gaatggtctgtctcagcaggtcaacagagttcacatcacccgcagctcccaagagcacgtgcc 1560
Db 1501 GAATGCTGCTTCGACGGTCAACGAGTTCACATCACCGCGACGTCCTCAAGAGCACGTGTC 1560
QY 1561 tgcctccgatttcaatctgagggaccctcgtctggaagagagagagcactcgcttcgagc 1620
Db 1561 TGCTCCGATTTCAATCTGGAGCACCTCGCTGGCAGAGCGAGAGCCACTGCGTTCCGAGC 1620
QY 1621 cacaacgaatgacatgagcgqgcagacaacacagcagatccagagagcattcaacacagcgc 1680
Db 1621 CACACGAATGGATGGAGCGGCACAAACAGCAGATCCAGGAGGCATTCAACCCAGCGC 1680
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Db 1681 TACAAGGACACAGCAGCTGCCAACGGAGCAGCCAACTCGACCATGCTCCATCTGGAGCGC 1740
QY 1741 gatgtttggagagacagctgagaacaatacacccgggtgcgggtcgctgaagaagtctct 1800
Db 1741 GATGTTTGGAGGAGCAGCTGAGAAACAATACCGGGTGCCTGCTCAAGAAAGTTCT 1800
QY 1801 ccatcgcgatggtctgcagctgttcccttcagaagaagcacccctcgaggatc 1860
Db 1801 CCATCCCGATGCTCTGGACGCTGTTCCTTCCCAAGAGACACCCCTCGCAGGATC 1860
QY 1861 tggagcgaagtgttcgtggtctcggtaccgcaggggtgtcatctcgaggaagccagat 1920
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QY 1921 cccctgagactactacatcaacacggttcacgagcgagcggtccagtcaactctattgagca 1980
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BASE COUNT

813 a 1038 c 949 g 768 t

RESULT 2

DMU55321

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DEFINITION

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LOCUS

DEFINITION

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Db 2398 TGGAGCAGACGACCATTCGGATCTGATTCGTCGCTCGAG 2438

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AC013909
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DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces.
ACCESSION AC013909
VERSION AC013909.1 GI:6437426
KEYWORDS HTG; HTGS, PHASE2.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 21163)
Adams, M. and Venter, J. C.
Direct Submission
Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10210421 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
1. 21163
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
BASE COUNT 5978 a 4746 c 4670 g 5769 t
ORIGIN

Query Match 52.5%; Score 1282.2; DB 58; Length 21163;
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Matches 1298; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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Db 4842 ATCTGAGCATGTACCCTGTGGAGCGGCTCCCATTCCTCCAGCCGGAAGAGGCATTCCTCCG 4901
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DEFINITION AB008537
ACCESSION AB008537
VERSION AB008537.1 GI:3043543
KEYWORDS CTBAK.
SOURCE Mus musculus
ORGANISM Mus musculus heart cDNA to mRNA.
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1888)
AUTHORS Fujita,A., Horio,Y. and Kim,D.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-1997) to the DDBJ/EMBL/GenBank databases. Akikazu
Fujita, Osaka University, Faculty of Medicine, Department of
Pharmacology II; Yamada-oka 2-2, Suita, Osaka 565, Japan
(E-mail:afujita@med.id.yamagata-u.ac.jp, Tel:81-6-879-3512,
Fax:81-6-879-3519)
2 (sites)
AUTHORS Kim,D., Fujita,A., Horio,Y. and Kurachi,Y.
TITLE Cloning and functional expression of a novel cardiac two-pore
background K+ channel (CTBAK-1)
JOURNAL Circ. Res. 82 (4), 513-518 (1998)
MEDLINE 98165556
COMMENT On Apr 10, 1998 this sequence version replaced gi:2589004.
Sequence updated (07-Apr-1998).
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University, 333 Cedar St., New Haven, CT 06520, USA
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RESULT 9
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ACCESSION AB013345
VERSION AB013345.1 GI:3149958
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SOURCE Mus musculus
ORGANISM Mus musculus cDNA to mRNA.
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2009)
AUTHORS Fujita,A., Horio,Y. and Kurachi,Y.
TITLE Direct Submission
JOURNAL Submitted (23-APR-1998) to the DDBJ/EMBL/GenBank databases. Akikazu
Fujita, Osaka University, Faculty of Medicine, Department of
Pharmacology II; Yamada-oka 2-2, Suita, Osaka 565, Japan
(E-mail:afujita@med.id.yamagata-u.ac.jp, Tel:81-6-879-3512,
Fax:81-6-879-3519)
2 (bases 1 to 2009)
AUTHORS Fujita,A., Horio,Y. and Kurachi,Y.
TITLE Mouse CTBAK
JOURNAL Published Only in DataBase (1998) In press
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ORIGIN

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Best Local Similarity 58.8%; Pred. No. 0.0083;
Matches 97; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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RESULT 9
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LOCUS Mus musculus mRNA for CTBAK, complete cds.
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KEYWORDS CTBAK.
SOURCE Mus musculus
ORGANISM Mus musculus cDNA to mRNA.
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2009)
AUTHORS Fujita,A., Horio,Y. and Kurachi,Y.
TITLE Direct Submission
JOURNAL Submitted (23-APR-1998) to the DDBJ/EMBL/GenBank databases. Akikazu
Fujita, Osaka University, Faculty of Medicine, Department of
Pharmacology II; Yamada-oka 2-2, Suita, Osaka 565, Japan
(E-mail:afujita@med.id.yamagata-u.ac.jp, Tel:81-6-879-3512,
Fax:81-6-879-3519)
2 (bases 1 to 2009)
AUTHORS Fujita,A., Horio,Y. and Kurachi,Y.
TITLE Mouse CTBAK
JOURNAL Published Only in DataBase (1998) In press
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BASE COUNT 312 a 647 c 548 g 381 t
ORIGIN
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TITLE      Trek-1 like two pore potassium channel
JOURNAL    Patent: WO 937762-A 29-JUL-1999;
           SMITHKLINE BEECHAM PLC (GB)
FEATURES   Location/Qualifiers
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BASE COUNT 335 a 280 c 302 g 329 t
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Best Local Similarity 58.4%; Pred. No. 0.012;
Matches 97; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 471 tgccttcttcttcgaccttgcacggttgctccacggtggatgggaatatatcgccaac 530
Db 401 TTCCTCTCTCTTCTGCGCACTGTTATTACAACCATAGGATTTGGAAACATCTCACCACG 460

Qy 531 caccttcgcgcgagcatgatcatgcggtatctgcgtgattgcgtgacatcccgccaatgg 590
Db 461 CACAGAAGGGCGGCAAAATATTTCTATCATCTATGCTTACTGCGAATTCCTCTTTGG 520

Qy 591 tctctcttgcgcgcctgcgcaatactttggacgtacgtttgaa 636
Db 521 TTTTCTCTGCTGAGTGGAGATCAGCTAGGACCATATTTGGA 566

RESULT 13
AF171068 1252 bp mRNA PRI 01-AUG-2000
LOCUS Homo sapiens two-pore domain potassium channel TREK-1 (TREK-1)
DEFINITION mRNA, complete cds.
ACCESSION AF171068
VERSION AF171068.1 GI:9622334
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1252)
AUTHORS Meadows,H.J., Benham,C.D., Cairns,W., Gloger,I.S., Jennings,C.,
Meahurst,A.D., Murdoch,P. and Chapman,C.G.
TITLE Cloning, localization and functional expression of the human
ortholog of the TREK-1 potassium channel
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1252)
AUTHORS Chapman,C.G., Gloger,I.S. and Meadows,H.J.
TITLE Direct Submission
JOURNAL Submitted (22-JUL-1999) Biotechnology & Genetics, SmithKline
Beecham Pharmaceuticals, New Frontiers Science Park (North), Third
Avenue, Harlow, Essex CM19 5AW, UK
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              1..1252
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CVLFVALPILFIKHIQSGSALDAIYFVVIITTTIGFDYVAGGSDIEYLDYFKPVWVF
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BASE COUNT 335 a 282 c 303 g 332 t
ORIGIN

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Best Local Similarity 58.4%; Pred. No. 0.012;
Matches 97; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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Db 407 TTCCTCTCTCTTCTGCGCACTGTTATTACAACCATAGGATTTGGAAACATCTCACCACG 466

Qy 531 caccttcgcgcgagcatgatcatgcggtatctgcgtgattgcgtgacatcccgccaatgg 590
Db 467 CACAGAAGGGCGGCAAAATATTTCTATCATCTATGCTTACTGCGAATTCCTCTTTGG 526

Qy 591 tctctcttgcgcgcctgcgcaatactttggacgtacgtttgaa 636
Db 527 TTTTCTCTGCTGAGTGGAGATCAGCTAGGACCATATTTGGA 572

RESULT 14
AF004711 2106 bp mRNA PRI 05-JAN-1999
LOCUS Homo sapiens two-pore potassium channel TPKC1 mRNA, complete cds.
DEFINITION AF004711
ACCESSION AF004711
VERSION AF004711.1 GI:4101565
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2106)
AUTHORS Price,L.A., Hellings,S.E., Hayashi,J.H. and Pausch,M.H.
TITLE TPKC1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2106)
AUTHORS Price,L.A., Hellings,S.E., Hayashi,J.H. and Pausch,M.H.
TITLE Direct Submission
JOURNAL Submitted (19-MAY-1997) Cyanamid Agricultural Research Center,
American Cyanamid Company, PO Box 400, Princeton, NJ 08543-0400,
USA.
FEATURES   Location/Qualifiers
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GNISPRTEGGKIFCIYALLGIPLGFLAGVGDLGTFIGKIAKVEDTIFIKWNVSQ
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SDIEYLDYFKPVWVFVILVGLAYFAAVLSMIGRLVRVSKTKKEVGEFRAHAAMT
NVTAEKTRRLSVEIYDKFORATSIKRLSAELAGNHNQELTPCRRLTSVNHILTSE
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BASE COUNT 552 a 471 c 486 g 581 t 16 others
ORIGIN

Query Match      2.3%; Score 55.6; DB 10; Length 2106;
Best Local Similarity 58.4%; Pred. No. 0.012;
Matches 97; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 471 tgccttcttcttcgaccttgcacggttgctccacggtggatgggaatatatcgccaac 530
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2001, 16:11:22 ; Search time 122.06 Seconds
(without alignments)
7512.638 Million cell updates/sec

Title: US-08-816-011c-1
Perfect score: 2441
Sequence: 1 acgcagccgcgcgagtgta.....atctgattcgtgcgctcgag 2441

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2441	100.0	2441	17 T33201	DmORF1 potassium c
2	55.6	2.3	321	20 Z00041	Partial h-TREK1 po
3	55.6	2.3	1246	20 Z00039	h-TREK1 polynucleo
4	55.6	2.3	3300	20 Z11915	Human potassium ch
5	54.6	2.2	1182	21 A27105	Human h-TRAAK cDNA
6	54.6	2.2	1218	21 A27106	Human h-TRAAK cDNA
7	53.4	2.2	1551	21 Z98176	Human signal pepti
8	52.4	2.1	1794	20 Z10606	cDNA encoding a me
9	52.2	2.1	1993	20 Z10607	cDNA encoding a me
10	52.2	2.1	1994	20 Z00040	Mouse h-TREK1 poly
11	49	2.0	2180	20 X78383	Human hTREK-1 cDNA
12	49	2.0	2571	20 Z11914	Human potassium ch

13	49	2.0	2671	21	246092	CDNA encoding KT4,
14	49	2.0	2735	21	246094	CDNA encoding KT5,
15	45.4	1.9	1894	18	T64960	TWIK-1 potassium c
16	41.8	1.7	1011	17	T33202	F22b7.7 potassium
17	41	1.7	3480	21	A07601	Long QT syndrome a
18	41	1.7	3950	21	A07602	Long QT syndrome a
19	41	1.7	10732	21	A10594	Gene encoding a su
20	40.6	1.7	1497	21	A15943	Human protein clon
21	40.6	1.7	3768	21	A15953	Human protein clon
22	39.2	1.6	1658	21	Z87209	Human TRAP cDNA cl
23	38.8	1.6	3141	20	X56415	Human erg subfamil
24	37.8	1.5	12474	20	X78131	Plasmid pMP76 DNA.
25	37.6	1.5	3742	21	Z93334	Rat eikl potassium
26	36.8	1.5	756	21	A02602	Human colon cancer
27	36.6	1.5	1981	21	Z51194	Human ischaemic he
c 28	36.6	1.5	2017	20	V08830	Gene No. 20 encodi
c 29	36.4	1.5	1801	21	A09381	Human DNA encoding
30	36.4	1.5	3424	20	Z11901	Human potassium ch
31	36	1.5	296	16	T25865	Human gene signatu
c 32	36	1.5	49272	19	V35000	Mycobacteriophage
c 33	35.8	1.5	2381	15	Q44449	3-acylating enzyme
34	35.8	1.5	2814	20	X57141	Mouse KCNQ3 cDNA.
35	35.8	1.5	2886	21	Z35716	Human potassium io
36	35.8	1.5	2967	21	Z35717	Human potassium io
37	35.8	1.5	3002	21	Z35721	Human eag related
38	35.8	1.5	3083	21	Z35722	Human eag related
39	35.8	1.5	30001	18	T61016	Total DNA sequence
40	35.8	1.5	30001	20	X05110	S. aureofaciens DN
41	35.6	1.5	516	19	V47574	Leishmania antigen
42	35.6	1.5	1170	21	A23431	CDNA encoding huma
c 43	35.4	1.5	348	14	Q61357	Human brain Expres
c 44	35.4	1.5	2008	21	Z51193	Human ischaemic he
c 45	35.4	1.5	2974	16	Q79630	Partial FRAXE regi

ALIGNMENTS

RESULT 1

T33201	ID	T33201 standard; cDNA; 2441 BP.
XX	XX	T33201;
AC	XX	T33201;
XX	XX	16-OCT-1996 (first entry)
XX	XX	DmORF1 potassium channel gene.
DE	DE	DmORF1; potassium channel; fruitfly; polyadenylation site;
XX	KW	potassium dependence; Saccharomyces cerevisiae; potassium-agonist;
KW	KW	potassium-antagonist; drug screening; insecticide; cardiac disorder;
KW	SS	ss.
OS	OS	Drosophila melanogaster.
XX	XX	Key
XX	XX	Location/Qualifiers
FT	FT	190..2046
FT	FT	/*tag= a
FT	FT	/product= Potassium channel DmORF1 protein
FT	FT	polyA_signal
FT	FT	2093..2098
FT	FT	/*tag= b
XX	XX	WO9613520-A1.
PN	PN	09-MAY-1996.
XX	XX	25-OCT-1995; 95WO-US14364.
XX	XX	31-OCT-1994; 94US-0332312.
XX	XX	(AMCY) AMERICAN CYANAMID CO.
XX	XX	Pausch MH, Price LA;
PI	PI	


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Db 1681 tacaaggagacagcagcgtgcgaacgagagcagccaaactcgacacatggtccatctggagcgc 1740
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Db 1741 gatgctttggaggagcagctgagaacaatacaccgggtgcccgtgcgctcaagaagtctct 1800
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Db 1861 tggagcgcaagtgtccgtggtctcgttacccgaggggtgatctcgcaggaagccagat 1920
Qy 1921 cccgcgtggaactactatcaacacgggtcaccgggcccctccagtcacatctctatttgcga 1980
Db 1921 cccgcgtggaactactatcaacacgggtcaccgggcccctccagtcacatctctatttgcga 1980
Qy 1981 acgagcgcgttccgcaccgccttcgaatcgaatggagcgttggcagcgcggcggcgcg 2040
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Db 2341 cctctgctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2400
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RESULT 2

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ID Z00041 standard; DNA; 321 BP.
XX
AC Z00041;
XX
DT 12-OCT-1999 (first entry)
XX
DE Partial h-TREK1 polynucleotide.
XX
KW partial h-TREK1; two pore potassium channel; inflammatory disease;
KW chromosome lq32; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..321
FT /product= "partial h-TREK1 polypeptide"
FT /transl_except= (pos:4..6, aa:Ser)
FT /transl_except= (pos:13..15, aa:Val)
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XX WO9937762-A1.
PN
XX 29-JUL-1999.
PD
XX
PF 02-DEC-1998; 98WO-EP07805.
XX
PR 09-OCT-1998; 98GB-0022135.
PR 27-JAN-1998; 98EP-0300570.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Chapman CG, Meadows HJ;
XX
DR WPI; 1999-469126/39.
XX
P-PSDB; Y28498.
XX
PT New two pore potassium channel used for, e.g. treatment of cancer,
PT pulmonary, cardiovascular and inflammatory diseases
XX
PS Claim 18; Page 24; 44pp; English.
XX
CC This sequence is a partial h-TREK1 polynucleotide, encoding the h-TREK1
CC polypeptide Y28498. Z00039 and Y28496 are complete h-TREK1 polynucleotide
CC and polypeptide sequences. h-TREK1 is a two pore potassium channel, and
CC the gene maps to human chromosome lq32, between the markers D15237 and
CC W15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a
CC disease or susceptibility to a disease related to expression or activity
CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the
CC treatment of diseases including cancer, pulmonary, cardiovascular, and
CC inflammatory diseases, pain, psychiatric disorders, including depression
CC and schizophrenia, neurodegenerative diseases including Alzheimer's,
CC stroke, and head trauma and neurological disorders including migraine.
XX
SQ Sequence 321 BP; 86 A; 67 C; 66 G; 102 T; 0 other;

Query Match 2.3%; Score 55.6; DB 20; Length 321;
Best Local Similarity 58.4%; Pred. NO. 9.4e-06;
Matches 97; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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Db 39 tctctctcttgcctcaccggttgcacacggtgggataatggaatataatcgcacac 98
Qy 531 cactctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 590
Db 99 cacagaaaggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 158
Qy 591 tatectcttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 636
Db 159 tttctctctgctggagtggtggagatcagtcagtcagtcagtcagtcagtcagtcagtcagtc 204

RESULT 3
200039
ID Z00039 standard; DNA; 1246 BP.
XX
AC Z00039;
XX
DT 12-OCT-1999 (first entry)
XX
DE h-TREK1 polynucleotide.
XX
KW h-TREK1; two pore potassium channel; inflammatory disease;
KW chromosome lq32; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 9..1244
FT /product= "a
FT /tag= "h-TREK1"
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XX AC Z10606;
XX DT 18-NOV-1999 (first entry)
XX DE cDNA encoding a mechanically sensitive potassium channel protein TRAAK.
XX KW Mechanically sensitive potassium channel protein; TRAAK;
KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;
XX KW muscular disease; ds.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 284..1480
XX FT /*tag= a
XX PW WO9945108-A2.
XX PD 10-SEP-1999.
XX PF 23-FEB-1999; 99WO-FR00404.
XX PR 05-MAR-1998; 98FR-0002725.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;
XX DR WPI; 1999-551038/46.
XX DR P-PSDB; Y30647.
XX PT New mechanically sensitive potassium channel, used to screen for
XX PT specific modulators, potential therapeutic agents for heart and nervous
XX PT system disorders
XX PS Claim 6; Fig 1; 40pp; French.
XX XX The present sequence encodes a mechanically sensitive potassium
XX CC channel protein designated TRAAK. The protein is activated by
XX CC polyunsaturated fatty acids, particularly arachidonic acid, and by
XX CC riluzole. The protein is used to screen for specific modulators which
XX CC are useful for treating or preventing diseases of the heart and nervous
XX CC systems in humans and animals, e.g. epilepsy, cardiovascular disease
XX CC (arrhythmia), neurodegeneration (particularly where associated with
XX CC ischemia or anoxia), abnormalities of hormone secretion and muscular
XX CC disease. The protein itself may be used to treat these diseases.
XX CC Antibodies specific for the protein are used to detect it in tissues,
XX CC also as therapeutic inhibitors or activators.
XX SQ Sequence 1794 BP; 348 A; 574 C; 494 G; 378 T; 0 other;

Query Match 2.13; Score 52.4; DB 20; Length 1794;
Best Local Similarity 48.4%; Pred. NO. 0.00017;
Matches 242; Conservative 0; Mismatches 246; Indels 12; Gaps 3;

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Qy 515 ggaatataatcgcaacacaccttcgctgacgagatgatcatgctgctggtgattg 574
Db 606 gcaatataatgattacacagatgacggcgctctctttgtatcttctatgcactggtgg 665
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Qy 935 tgtggttcatcttctcgtcg 954
Db 1014 tagcctactcgcctcagtg 1033

RESULT 9
#Z10607
ID Z10607 standard; cDNA; 1993 BP.
XX AC Z10607;
XX DT 18-NOV-1999 (first entry)
XX DE cDNA encoding a mechanically sensitive potassium channel protein TREK-1.
XX KW Mechanically sensitive potassium channel protein; TREK-1;
KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;
XX KW muscular disease; ds.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 484..1596
XX FT /*tag= a
XX PN WO9945108-A2.
XX PD 10-SEP-1999.
XX PF 23-FEB-1999; 99WO-FR00404.
XX PR 05-MAR-1998; 98FR-0002725.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;
XX DR WPI; 1999-551038/46.
XX DR P-PSDB; Y30648.
XX PT New mechanically sensitive potassium channel, used to screen for
XX PT specific modulators, potential therapeutic agents for heart and nervous
XX PT system disorders
XX PS Claim 7; Page 23-25; 40pp; French.
XX XX The present sequence encodes a mechanically sensitive potassium
XX CC channel protein designated TREK-1. The protein is activated by
XX CC polyunsaturated fatty acids, particularly arachidonic acid, and by
XX CC riluzole. The protein is used to screen for specific modulators which
XX CC are useful for treating or preventing diseases of the heart and nervous
XX CC systems in humans and animals, e.g. epilepsy, cardiovascular disease
XX CC (arrhythmia), neurodegeneration (particularly where associated with

```


OS Homo sapiens.

PN EP930364-A1.

AA 30-NOV-1999 (first entry)

Human potassium channel K+Hnov49 cDNA.

Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome; kw
cardiovascular disorder; CNS disorder; renal disorder. ds.

cardiovascular disorder; CNS disorder; renal disorder; ds:
XX
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US
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nomu saprens.

EH	Key	Location/Qualifiers
ET	CDS	110 1295

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PS Claim 5: page 15-18: 21pp: English:

SQ Sequence 2180 BP; 374 A; 669 C; 645 G; 492 T; 0 other:

Qy 446 cggcctacacgctggagccttctaccatgacctctctctcggccttcaccttcacctccacga 505

CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
CC As potassium channels are critical components of virtually all cells,
CC it is likely that abnormal potassium channels are also implicated in

CC certain renal, cardiovascular and central nervous system (CNS) disorders.
CC Nucleotides encoding kHnov proteins may be used for identifying
CC homologous or related proteins and the DNA sequences encoding them. They
CC may be used to produce compositions that modulate the expression and
CC function of the kHnov protein and in studying the biochemical pathways
CC associated with it. They may also be used for the recombinant production
CC of kHnov protein in fermentation cultures. Additionally, such
CC nucleotides may be used in gene therapy protocols for the treatment
CC of diseases associated with abnormal potassium channels.
XX
XX Sequence 2571 BP: 488 A: 744 C: 774 G: 565 T: 0 other:
SQ

Claim 14; Fig 1A-C; 53pp; English.

The present sequence encodes a protein, designated KT4, which is a member of the TWIK family 2PD potassium channel polypeptides. These polypeptides contain two potential P-domains and 8 (preferably 4) transmembrane domains. The KT4 cDNA sequence was isolated from a brain cDNA library using degenerate oligonucleotides derived from human expressed sequence tag (EST) AA604914. The polypeptides and polynucleotides are used in the diagnosis, prevention and treatment of disease states. The polynucleotides may be used to detect and quantitate expression of TWIK family 2PD potassium channels, and aberrant or mutant forms of the polynucleotide which cause various diseases and disorders. Antisense oligonucleotides may be used to modulate the expression of polynucleotides of the invention. The polypeptides are used for treating diseases and disorders associated with ion channel dysfunction, including renal, musculoskeletal and proliferative diseases, e.g. renal failure, nephrosis, cirrhosis, dysphagia, gastritis, myotonias, muscular dystrophy, atherosclerosis and cancers.

Sequence 2671 BP: 563 A: 743 C: 798 G: 567 T: 0 other:

Search completed: March 17, 2001, 17:56:23
Job time: 6301 sec

532 acct+cccccccccat

Db 1322 accaactccgagaggtcttccatctcgtcatgctccatcggtccctgatgtaagcc 1381
 Qy 592 atctctttg 601
 Db 1382 agcatcttcg 1391

RESULT 6

US-08-614-770A-1/c
 ; Sequence 1, Application US/08614770A
 ; Patent No. 5773267
 ; GENERAL INFORMATION:
 ; APPLICANT: WILLIAM R. JACOBS AND GRAHAM F. HATFULL
 ; TITLE OF INVENTION: D29 SHUTTLE PHASMSIDS AND USES THEREOF
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
 ; STREET: 90 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10016

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
 MEDIUM TYPE: DISKETTE
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: ASCII

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/614,770A
 FILING DATE: MARCH 7, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: ELIZABETH A. BOGOSIAN
 REGISTRATION NUMBER: 39,911
 REFERENCE/DOCKET NUMBER: 96700/402
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 697-5995
 TELEFAX: (212) 286-0854 or 286-0082
 TELEX: TWX 710-581-4766
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 49272
 TYPE: NUCLEIC ACID
 STRANDEDNESS: DOUBLE
 TOPOLOGY: LINEAR

MOLECULE TYPE: OLIGONUCLEOTIDE
 DESCRIPTION: NO
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: MYCOBACTERIOPHAGE
 INDIVIDUAL ISOLATE: D29
 US-08-614-770A-1

Query Match 1.5%; Score 36; DB 1; Length 49272;
 Best Local Similarity 51.2%; Pred. No. 14;
 Matches 84; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Qy 1600 gagaggccactgcgttcagcacaacgaatggacatggagcgcagacagcagatc 1659
 Db 42506 GAGATCCCGATCCCGGTTCAACTACAAAGGCATCTCGTGTGGAGAGATCGAAGACCC 42447
 Qy 1660 cagaggcattcaaccagcgtacaagggacagagcgtgccaagcggagcagccaactcg 1719
 Db 42446 CTCGAGCGGTACGAGCGGCTCTACGAGGACTTCCTCGCGCTGATCGTGTGGAACAATC 42387
 Qy 1720 accatggtccatctggagcccgatgctttggaggagcagctgag 1763
 Db 42386 ACCAAGTCCCGACCGGATCGGGGACCGGGATGACCCGTTTCAG 42343

RESULT 7

US-08-125-468-1
 ; Sequence 1, Application US/08125468
 ; Patent No. 5589385
 ; GENERAL INFORMATION:
 ; APPLICANT: Ryan, Michael J.
 ; APPLICANT: Lotvin, Jason A.
 ; APPLICANT: Strathy, Nancy
 ; APPLICANT: Fantini, Susan E.
 ; TITLE OF INVENTION: Cloning of the biosynthetic pathway for
 ; TITLE OF INVENTION: chlortetracycline and tetracycline formation and cosmid
 ; TITLE OF INVENTION: useful therein
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: American Cyanamid Company
 ; STREET: One Cyanamid Plaza
 ; CITY: Wayne
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07470

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/125,468
 FILING DATE: 22-SEP-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Tsevdos, Estelle J
 REGISTRATION NUMBER: 31,145
 REFERENCE/DOCKET NUMBER: 31,255-02
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201)831-3241
 TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30001 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-125-468-1

Query Match 1.5%; Score 35.8; DB 1; Length 30001;
 Best Local Similarity 46.9%; Pred. No. 12;
 Matches 112; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

Qy 756 ggtgctgcctcgtggtgttcaactacttcgagaactggggcctatcttccatctcgt 815
 Db 10124 GGTGCTGCGGTGGGCGAGCGCGGTGAGATCCAGGTCGGGGCGCCGAGTGTGATCTGGG 10183
 Qy 816 gtactacagctatgaccacacacaaatggattcgggtgactatgccccacattgg 875
 Db 10184 CTACCTGGCGACGGGCCACCGCGCTCGACGCGGACGCGCTGGTTCGCGACCGGTGA 10243
 Qy 876 agccaacagcccaaggaggtcggcggttctggtgtctatcagatctttgtatcgt 935
 Db 10244 CGTCGGCGGATCGACGAGCGCGCGCTGTGTCGTCGACCGGATCAAGAGAGTCTT 10303
 Qy 936 gtggttcctctcgtcgggatatcttctgtatgatcatcattatcactcggggcc 994
 Db 10304 CAAGTGCACAACTGCGTGTGCTGCCCGACCGAGATCGAGCGGTGCTGATCGCGCAC 10362

RESULT 8

US-08-474-933-1
 ; Sequence 1, Application US/08474933
 ; Patent No. 5866410
 ; GENERAL INFORMATION:
 ; APPLICANT: Ryan, Michael J.

QY 2083 cgcacatcgccattggg 2098
DB 382 TGAGAGCGACGCGGG 367

RESULT 15

US-07-920-281C-1
; Sequence 1, Application US/07920281C
; Patent No. 5739026
; GENERAL INFORMATION:
; APPLICANT: Garoff, Henrik
; TITLE OF INVENTION: DNA Expression Systems Based on
; TITLE OF INVENTION: Alphaviruses
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/920.281C
; FILING DATE: 13-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 828-103P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Semliki Forest Virus
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..11517
; OTHER INFORMATION: /label= genome
; OTHER INFORMATION: /note= "Semliki Forest Virus complete nucleotide
; OTHER INFORMATION: sequence, presented as a cloned DNA sequence; see
; OTHER INFORMATION: Figure 5."
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 87..7379
; OTHER INFORMATION: /product= "SFV polyprotein"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7421..11179
; OTHER INFORMATION: /product= "SFV polyprotein"
US-07-920-281C-1

Query Match 1.4%; Score 34.4; DB 1; Length 11517;
Best Local Similarity 57.4%; Pred. No. 18;
Matches 62; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 17 tgatatatttttttagctcagttctcagttcttcgagttctctttaagagaaaaa 76

DB 11407 TTTTATTATTTTTCGAATGGTTTTTAATATTTTCAAAAAAAAAAAAAAAAAAAAA 11466
QY 77 aaataataagtcacaaactacaaacacacagcgaaagcgaaagcaac 124
DB 11467 AAC 11514

Search completed: March 17, 2001, 17:55:42
Job time: 6345 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2001, 15:52:47 ; Search time 1360.82 Seconds
(without alignments)
12569.831 Million cell updates/sec

Title: US-08-816-011C-1
Perfect score: 2441
Sequence: 1 acgcgacgcgcgcgagtgta.....atctgattcgtgcgctcgag 2441

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

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 156: em_estpl45:*
 157: em_estpl46:*
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 159: em_estpl48:*
 160: em_estpl49:*
 161: em_estpl50:*
 162: em_estpl51:*
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 164: em_estpl53:*
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 179: em_estpl68:*
 180: em_estpl69:*
 181: em_estpl70:*
 182: em_estpl71:*
 183: em_estpl72:*
 184: em_estpl73:*
 185: em_estpl74:*
 186: em_estpl75:*
 187: em_estpl76:*
 188: em_estpl77:*
 189: em_estpl78:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	549.8	22.5	582	8	AA539933	AA539933 LD19236.5
2	470.2	19.3	487	20	AI405401	AI405401 GH25390.5
3	148.2	6.1	569	18	AI293134	AI293134 GH18237.5
4	56.2	2.3	483	19	AI323858	AI323858 mf89d07.y
5	56.2	2.3	677	22	AI605559	AI605559 ma07h04.y
6	56.2	2.3	925	190	CNS0091P	AL053013 Drosophila
7	55.6	2.3	401	7	AA464375	AA464375 z81d11.r
8	55.6	2.3	925	190	CNS0091P	AL053013 Drosophila
9	54.6	2.2	318	147	W99136	W99136 mf89d07.r1
10	54.6	2.2	671	91	AW506290	AW506290 GE1674.G1
11	48.2	2.0	590	138	BE981482	BE981482 UI-M-CG0p
12	48.2	2.0	593	138	BE981393	BE981393 UI-M-CG0p
13	47.4	1.9	389	23	AI687362	AI687362 tp95a05.x
14	47.4	1.9	941	135	BE735881	BE735881 601305237
15	47.2	1.9	935	190	CNS0163Z	AL108265 Drosophila
16	46.2	1.9	1101	190	CNS0175Y	AL108460 Drosophila
17	45.1	1.8	1101	190	CNS0160E	AL107216 Drosophila
18	44.8	1.8	337	108	BE466893	BE466893 hz28d11.x
19	44.8	1.8	436	27	AI968607	AI968607 wt90e12.x
20	44.8	1.8	457	23	AI690321	AI690321 tz15g05.x
21	44.6	1.8	653	191	CNS02MID	AL203530 Tetraodon
22	44.4	1.8	908	190	CNS01678	AL108382 Drosophila
23	44.2	1.8	433	40	AW141778	AW141778 EST291867
24	44.2	1.8	839	190	CNS004NB	AL054280 Drosophila
25	43.8	1.8	586	111	BE680493	BE680493 df81b01.y
26	43.6	1.8	419	110	BE640340	BE640340 946084A02
27	43.6	1.8	1101	193	CNS05C4L	AL330654 Tetraodon
28	43.4	1.8	607	37	AV612885	AV612885 AV612885
29	43.4	1.8	632	93	AW644141	AW644141 cm37h03.w
30	43.2	1.8	368	24	AI739096	AI739096 w17h03.x
31	43.2	1.8	844	190	CNS0052P	AL056652 Drosophila
32	43.2	1.8	1124	191	CNS02Y0X	AL219930 Tetraodon
33	43.2	1.8	1008	191	CNS035YI	AL223347 Tetraodon
34	42.6	1.7	518	111	BE720244	BE720244 RCO-HF088
35	42.4	1.7	531	22	AI586911	AI586911 486057H11
36	42.4	1.7	594	20	AI444765	AI444765 486013C05
37	42.4	1.7	619	22	AI603727	AI603727 486082G10
38	42.2	1.7	369	5	AA308453	AA308453 EST179278
39	42.2	1.7	957	190	CNS015W7	AL105985 Drosophila
40	42.2	1.7	1011	192	CNS04LCX	AL295962 Tetraodon
41	42.2	1.7	237	25	AI804983	AI804983 tx03g04.x
42	42.2	1.7	417	140	C89710	C89710 C89710 Dict
43	41.8	1.7	380	97	AW952265	AW952265 EST364335
44	41.8	1.7	712	134	BE038709	BE038709 AB04D10.A
45	41.8	1.7	1039	191	CNS02ADN	AL188420 Tetraodon

ALIGNMENTS

RESULT 1
 AA539933
 LOCUS
 DEFINITION
 LD19236.5prime LD Drosophila melanogaster embryo Bluescript
 Drosophila melanogaster cDNA clone LD19236 5prime, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 AA539933 582 bp mRNA
 EST
 27-NOV-1998
 AA539933.1 GI:2795149
 EST.
 fruit fly.

BASE COUNT	113 a	215 c	210 g	136 t	3 others
ORIGIN					
Query Match	2.3%;	Score 56.2;	DB 22;	Length 677;	
Best Local Similarity	58.8%;	Pred. No. 0.00034;			
Matches	97;	Conservative 0;	Mismatches 68;	Indels 0;	Gaps 0;
QY	456	gtgagacctttacatcgctttcttcttcgcttcgcgccttcacgcgtttgtctccacggtgggatattgg	515		
Db	221	GTGGCGCTTCGCGGCTCTTCTACTTCGCGCATCACCGTCATCACCACTCGCGCTATGG	280		
QY	516	gaatatatcgcaaacacccttcgcgcgacggatgatcatgatcgcgtattcgttgattgg	575		
Db	281	TCATCGCGCGCCAGCAGCAGGAGCGCAAGTGTTCGTGATGTTCACGCGCTGCTGGG	340		
QY	576	catcccgctcaatgggtatcctcttttcgcgccttcgcgcgcgaatacctt	620		
Db	341	CATCCCGCTCACACTAGTCTATGTTCCAGAGCGCTGGGTGACCCAT	385		
RESULT	6				
CNS0091P		925 bp	DNA	GSS	03-JUN-1999
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
FEATURES					
source					
BASE COUNT	120 a	61 c	61 g	172 t	511 others
ORIGIN					
Query Match	2.3%;	Score 56;	DB 190;	Length 925;	
Best Local Similarity	13.7%;	Pred. No. 0.00041;			
Matches	53;	Conservative 175;	Mismatches 160;	Indels 0;	Gaps 0;
QY	1887	gtaccggagggtgtcattctcgcaagaagcagatccctcgctggactactatcaaacg	1946		

Db 538 GKKGSTTBGTTTTTTTSSGSGYKGCSSGSGBSGCCSCSSSSSSSCSCBCCCCSCS 597
 QY 1947 gtcaagcgccctccagtcatactatttgcgaacgagcggttcgcccacgccttc 2006
 Db 598 SYCCSSBSKCSNBSBSCCCSCSSKSVCTSCSSSSSSSSSTSSSTSSSTSSKSS 657
 QY 2007 gaatcaatggcagcttggccagcgcgcgcggttaacgaacatgggctccagatg 2066
 Db 658 SSGSSSSSSSYTTKSTASGSGSWAGGCGSTGTSSSSSSSSTSSSTSSSVSGSKS 717
 QY 2067 gaggatggaacaccccgccatcggttggcggttgagcgtatcaacgcaagcggtc 2126
 Db 718 STBSSBSBSSSSSSSTSSBSCSTSSSSSSSSSTSCCTCCCSYSYSSSTSSSS 777
 QY 2127 gctggcaagcgcgagcgagatcatcaccccaagaatacaagcccatcgctcgccg 2186
 Db 778 STWGSTGSSSSSVGTSSSDSTSCCCCYMCVCCSYBMCVTSYSCGSSSSSGK 837
 QY 2187 ggcagcatgtatccgcgacccgcgcgcttggccagatcgagatcgagcggcagc 2246
 Db 838 GGVTKCGCGCGSSSTNGMBGTSSACSSSSSSSCSSSVSSSSKSSASSSSVSSSGSGVS 897
 QY 2247 ttggcaaccagtggtctggtgagcgcg 2274
 Db 898 SNSSASKSSSSGSGSGSGSGSVSG 925

 RESULT 7
 LOCUS AA464375 401 bp mRNA EST 10-JUN-1997
 DEFINITION zx81d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
 IMAGE:810165 5' similar to TR:G1086491 G1086491 TWIK-1. ; mRNA
 sequence.
 ACCESSION AA464375
 VERSION AA464375.1 GI:2189259
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 401)
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie,
 T., Waterston, R. and Wilson, R.
 TITLE WashU-Merck EST Project 1997
 JOURNAL Unpublished (1997)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 315.
 Location/Qualifiers
 1..401
 /organism="Homo sapiens"
 /db_xref="GDB:6040286"
 /db_xref="taxon:9606"
 /clone="IMAGE:810165"
 /clone_lib="Soares ovary tumor NbHOT"
 /sex="Female"
 /tissue_type="ovarian tumor"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer (5'
 TGTTACCAATCTGAGTCGACGCGCGCGGTCTTTTCTTTTCTTTT 3'),
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo."
 BASE COUNT 111 a 83 c 86 g 121 t
 ORIGIN

 Query Match 2.3%; Score 55.6; DB 7; Length 401;
 Best Local Similarity 58.4%; Pred. No. 0.00044;
 Matches 97; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

 QY 471 tgccttcttcttcgctccacggttgcctccacggtgggatatgggaatatatcgcaac 530
 Db 118 TTCTTCTTCTTCTTGTGGCACTGTTATTACACCATAGGATTTGGAACATCTCACCACG 177
 QY 531 caccctcgcggacgatgatcatcgatcgctattggtgattggcattccctcgaatgg 590
 Db 178 CACAGAAGCGCGCAAAATATTCTGTATCATCTATGCTTACTGGGAATTCCTCTTTGG 237
 QY 591 tatcctcttgcgcgctcgcggaatactttggacgtacgtttgaa 636
 Db 238 TTTTCTTCTTGGCTGGAGTTGGAGATCAGTAGCAGCCACCATATTTGGA 283

 RESULT 8
 LOCUS CNS0091P/c 925 bp DNA GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL053013
 VERSION AL053013.1 GI:4934461
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 925)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osogawa and
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 p1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 Location/Qualifiers
 1..925
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR19D16"
 /note="end : TET3"

 BASE COUNT 120 a 61 c 61 g 172 t 511 others
 ORIGIN

 Query Match 2.3%; Score 55.6; DB 190; Length 925;
 Best Local Similarity 12.3%; Pred. No. 0.00052;
 Matches 43; Conservative 168; Mismatches 139; Indels 0; Gaps 0;


```

Db 145 AAAAATTTTAAAAACCCCCCCCCCGGGGAAAAATAAAAAAGCGCCCCCCCC 204
Qy 137 tgtttattttttttc 153
Db 205 CTTTtttttttttttttc 221

RESULT 14
BE735881
LOCUS BE735881 941 bp mRNA EST 15-SEP-2000
DEFINITION 601305237F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639657 5',
mRNA sequence.
ACCESSION BE735881
VERSION BE735881.1 GI:10149873
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 941)
TITLE NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC342 row: j column: 10
High quality sequence stop: 669.
Location/Qualifiers
1. 941
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3639657"
/clone_lib="NIH_MGC_39"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies)."
```

Search completed: March 17, 2001, 17:04:13
Job time: 4286 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2001, 18:53:13 ; Search time 77.65 Seconds
(without alignments)
272.141 Million cell updates/sec

Title: US-08-816-011c-2

Perfect score: 3283

Sequence: 1 MSPNRWILLIPYISYLMFG.....DAVRHRPSNRMAWPAAPAAAG 618

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_36.*
- 1: /cgn2_2/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /cgn2_2/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /cgn2_2/gcgdata/geneseq/geneseq/AA1982.DAT.*
 - 4: /cgn2_2/gcgdata/geneseq/geneseq/AA1983.DAT.*
 - 5: /cgn2_2/gcgdata/geneseq/geneseq/AA1984.DAT.*
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 - 8: /cgn2_2/gcgdata/geneseq/geneseq/AA1987.DAT.*
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 - 10: /cgn2_2/gcgdata/geneseq/geneseq/AA1989.DAT.*
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 - 20: /cgn2_2/gcgdata/geneseq/geneseq/AA1999.DAT.*
 - 21: /cgn2_2/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3283	100.0	618	17 R97984	DmORF1 potassium c
2	301.5	9.2	398	20 Y30647	A mechanically sen
3	301	9.2	499	21 Y94875	Human protein clon
4	298.5	9.1	370	20 Y30648	A mechanically sen
5	298.5	9.1	411	20 Y28497	Mouse h-TREK1 poly
6	292.5	8.9	411	20 Y34133	Human potassium ch
7	292.5	8.9	411	20 Y28496	h-TREK1 polypeptid
8	286	8.7	393	21 Y94425	Human h-TRAAK poly
9	286	8.7	393	21 Y94426	Human h-TRAAK poly
10	239	7.3	336	18 W23397	Human h-TREK1 poly
11	231.5	7.1	394	21 Y87291	Human signal pepti
12	210.5	6.4	313	20 Y34132	Human potassium ch

13	210.5	6.4	313	20 Y25116	Human hTREK-1 prot
14	210.5	6.4	313	21 Y68737	KT4, a TWIK family
15	210.5	6.4	313	21 Y68738	KT5, a TWIK family
16	204.5	6.2	336	17 R97986	P22b7.7 potassium
17	169.5	5.2	107	20 Y28498	Partial h-TREK1 po
18	116.5	3.5	888	20 Y17399	Human erg subfamil
19	114	3.5	824	20 Y24001	A potassium channel
20	114	3.5	962	21 Y83032	Rat Eagl potassium
21	110.5	3.4	2019	16 R67913	Cardiac sodium cha
22	110.5	3.4	2466	16 R71498	Human protein tyro
23	110.5	3.4	2466	19 W75999	Intracellular prot
24	110	3.4	2270	16 R69604	Calcium channel al
25	109	3.3	1081	20 Y13443	Amino acid sequenc
26	109	3.3	1105	20 Y13442	Amino acid sequenc
27	109	3.3	2251	16 R71009	Human neuronal cal
28	109	3.3	2270	16 R71010	Human neuronal cal
29	107.5	3.3	383	19 W98461	H. pylori GPO 718
30	105.5	3.2	408	18 W20814	H. pylori cell env
31	102	3.1	962	21 Y49944	Human potassium io
32	102	3.1	989	21 Y49945	Human potassium io
33	101.5	3.1	354	19 W74521	Human ATP-sensitiv
34	101.5	3.1	364	19 W74518	Human ATP-sensitiv
35	101.5	3.1	390	18 W13103	Mouse ATP sensitiv
36	101.5	3.1	390	18 W17932	Human K-ATP channel
37	101.5	3.1	390	18 W17931	Mouse K-ATP channel
38	101.5	3.1	390	19 W74516	Mouse ATP-sensitiv
39	101.5	3.1	390	19 W74517	Human ATP-sensitiv
40	101	3.1	655	19 W75990	Human Kv potassium
41	100.5	3.1	390	18 W13102	Human ATP sensitiv
42	98.5	3.0	160	20 Y32009	Streptomyces livid
43	98.5	3.0	2020	11 R06584	Cardiac sodium cha
44	97.5	3.0	570	21 Y57377	Human KVLQT1 prote
45	97.5	3.0	581	18 W33355	Human KVLQT1 assoc

ALIGNMENTS

RESULT	1
ID	R97984
XX	R97984 standard; Protein; 618 AA.
AC	R97984;
DT	16-OCT-1996 (first entry)
DE	DmORF1 potassium channel protein.
XX	DmORF1; potassium channel; fruitfly; pore-forming domain;
KW	transmembrane helix; N-glycosylation site; potassium-agonist;
KW	potassium-antagonist; drug screening; insecticide; cardiac disorder.
XX	Drosophila melanogaster.
XX	
FT	Key
FT	Domain
FT	Location/Qualifiers
FT	6..27
FT	/note= "Transmembrane domain M1"
FT	Modified-site
FT	58..60
FT	/note= "N-glycosylation site"
FT	Domain
FT	95..111
FT	/note= "Pore-forming domain H5-1"
FT	Domain
FT	120..140
FT	/note= "Transmembrane domain M2"
FT	Domain
FT	171..191
FT	/note= "Transmembrane domain M3"
FT	Domain
FT	208..224
FT	/note= "Pore-forming domain H5-2"
FT	Domain
FT	242..263
FT	/note= "Transmembrane domain M4"
XX	
XX	WO9613520-AL.
XX	
PD	09-MAY-1996.

Db 7 lallalvlysgalvqaleqheqqaqkmdhgrdqfirdhpcvsqksledfiklilv 66
QY 52 BELGKNTTQDEILQRIQSDYCDKPVTLPTVDDTPYTWTFYHAFVFTVGVGNI 111
Db 67 ealgg-----anpetsywnssnhsawngsafstgitttgygni 110
QY 112 SPTFAGRMIMTAYSVIGPVNGILFAGLGEVFGRT-----FEALYRYKKYKMSD 164
Db 111 vhtdagrlfcfyalgplfmgllagvdrlgslrrgighlealfkw----- 161
QY 165 HVPVQLGLITWIALPGIALFVLPCVGVHLLRELGLSISLYSVVTTTTFGFGDY 224
Db 162 -hvpvgvlrsisavlligellvltptf-vfswmeswskleayfvltvtttvgfgy 219
QY 225 VFTGAPKPEFGVVFVQIFVIMFISGLYLVIMTFTIRGLQS-----KKLAYLE 278
Db 220 vpgdgtgnsq-----ayqplvfwilfayfasvlttgnwlravrrtraemgilt 273
QY 279 QOLSSNLKATQRIWSG-----VTXDVG 301
Db 274 aqaas-----wtgtvtarvtrdtg 292

RESULT 3
Y94875
ID Y94875 standard; Protein; 499 AA.
AC Y94875;
XX
DT 12-JUN-2000 (first entry)
DE Human protein clone HP10538.
XX
KW Human protein; hydrophobic domain; nutritional source; haematopoiesis;
KW cytokine production; cell proliferation; cell differentiation;
KW immune deficiency; infectious disease; autoimmune disorder; asthma;
KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
KW nervous system disorder; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;
KW coagulation disorder; myocardial infarction; inflammatory condition;
KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
KW nephritis; therapy.
XX
OS Homo sapiens.
XX
PN WO200005367-A2.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-JP03929.
XX
PR 24-JUL-1998; 98JP-0208820.
PR 27-AUG-1998; 98JP-0224105.
PR 25-AUG-1998; 98JP-0238116.
PR 09-SEP-1998; 98JP-0254736.
PR 29-SEP-1998; 98JP-0275505.
XX
PA (SAGA) SACAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
XX
PI Kato S, Kimura T;
XX
DR WPI; 2000-182694/16.
XX
PT Novel human proteins having hydrophobic domains useful for treating
PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
XX
PS Claim 1; Page 245-247; 351pp; English.
XX
XX This sequence represents a human protein of the invention, which has

CC hydrophobic domains. The DNA sequences can be used as a probe or as a
CC genetic marker. The protein can also be used as a marker, and to identify
CC potential genetic disorders. The DNA and protein can also be used as
CC nutritional sources or supplements. The protein exhibits cytokine, cell
CC proliferation, cell differentiation activities and induces production of
CC other cytokines in certain cell populations. The protein also exhibits
CC immune stimulating or immune suppressing activity. It can be used in the
CC treatment of various immune deficiencies and disorders, and to treat
CC infectious diseases caused by viral, bacterial, fungal or other
CC infections. The protein is also used for treating autoimmune disorders
CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid
CC arthritis. It is also useful in the treatment of allergic reactions and
CC conditions such as asthma, and in immune suppression after organ
CC transplantation. The protein is useful in regulation of haematopoiesis
CC and consequently in the treatment of myeloid or lymphoid cell
CC deficiencies. It is also used in compositions for tissue growth or
CC regeneration. The protein is also used in the treatment of osteoporosis
CC or osteoarthritis and in the treatment of periodontal disease and other
CC tooth repair processes. The protein is used in the treatment of nervous
CC system disorders such as Alzheimer's disease, Parkinson's disease, and
CC Huntington's disease. They are useful for protection or regeneration and
CC treatment of lung or liver fibrosis, reperfusion injury in various
CC tissues, and conditions resulting from systemic cytokine damage. They are
CC also used for promoting or inhibiting tissue differentiation. They are
CC also used as contraceptives since they exhibit activin or inhibin related
CC activities and as a fertility inducing therapeutic. They are used for
CC treating various coagulation disorders and in treatment and prevention of
CC conditions resulting from coagulation activities e.g. myocardial
CC infarction or stroke. They also acts as receptors, receptor ligands or
CC inhibitors or agonists of receptor/ligand interactions. They are used to
CC treat inflammatory conditions such as septic shock, sepsis, ischaemia
CC reperfusion injury, arthritis, and nephritis. They can be used to
CC prevent tumours.
XX
SQ Sequence 499 AA;

Query Match 9.2%; Score 301; DB 21; Length 499;
Best Local Similarity 24.6%; Pred. No. 2.6e-22;
Matches, 133; Conservative 93; Mismatches 22; Indels 88; Gaps 23;

QY 4 NRWILLIFYISLMFGAIIYHIEHGEKISRQKQAIINEVYLLLEELGDKNTTQD 63
Db 3 drgpltsaifylaigaafvelephwk-----eaknyttqkhlkfcplgqegid 58
QY 64 EILQRIQSDYCDKPVTLPTVDDTPYTWTFYHAFVFTVGVGNIPTTFAGRMIMI 123
Db 59 kilevvsdaagdvai--tgnqcfnnwnpnamifaatvittgynvapkpapgrfvcv 116
QY 124 AYSVICIPVNGILFAGLGEYFGRTFEALYRYKKYKMSDTHYVPPQLGLITWIALIP 183
Db 117 fyglfgvplcltwisalgkffg-----grakrlgqfltkrgvsirkaqitctvfiwv 169
QY 184 GIALFLVPCVGVHLLRELGLSSI-SLYSVYVTTTTFGFGDYVFTGAPKPEFGV 242
Db 170 gvlvhlvlpff-vfmvte-gwnyieglyysfistigfdvfa--gvnps---anyhal 222
QY 243 YOIFVIVWFIFSLGVLVIMTFT-----ITRGLQSKLAYLEQQLSS--NLKATONRIW 293
Db 223 yryfvelwiylglawlsifvwnkvmfvevhkaikrrrrrkesfessphskalqvk-g 281
QY 294 SGVTKDVGYLRRMLNELYILKVKPVVTDV--DIATYL-----PRSNSCP 335
Db 282 staskdvnifs-----flskkeetyndlikqkqkamktsgggetgpggpggggip 335
QY 336 DLSMRVVEPAPISRKRAFSVCADWVGQREAGMVHANSDDLTLKLDREKTEATAYHQ 395
Db 336 alppslv-plvvyknrv-ptleevsqtlrskghvsrpsdeavapadesspapevfmm 393
QY 396 TTDLLAKVVALATVKPPPAEOEDAAALYGYHG--FSDSQILASEWSFSFVNEFTSPRP 453
Db 394 qlidrise-----ecepwdagq-----yhlplfqdasitfvnteaglsdeets---- 435

Db	106	ivaainagiaplgnssnqvshwdlgssffagtvittigtfgnisprteggkfcilayall	165
Qy	129	GIPVNGILFAG----LGEYGRTRFEALYRRYKKYKMSTDMHYVPPOLGLITTTVIALIPG	184
Db	166	gipifgllagvgdqgtifgkgiakvedtfikwnvs-----qtkiriistiifilf-g	218
Qy	185	IALFLVLPCVGVHLLREL-GLSSI-SLYYSYVTTTTTIGFGDYVPTFGANPKKEFGGVVV	242
Db	219	cvlifaipav---ifkhiegwsaldalyfvvittittigtfgdyva-----ggsdle	265
Qy	243	YOIFV--IVVF--IFSILGYLVMTMTFITRGLQ--SKKLAYLEQQLSSNLKATONRIWSGV	296
Db	266	yltdfypvwwfwilvglayfaavlsimgdwlrvlisk-----tkeevgefrahawetany	321
Qy	297	TKDVGYLRLMLN-ELY 311	
Db	322	taefketrrrlsveiy 337	
RESULT	5		
Y28497			
ID	Y28497	standard; Protein; 411 AA.	
XX	Y28497;		
AC			
DT	12-OCT-1999	(first entry)	
DT			
DE	Mouse h-TREK1 polypeptide.		
XX			
KW	h-TREK1; two pore potassium channel; inflammatory disease;		
KW	chromosome 1q32.		
OS	Mus musculus.		
OS			
PN	WO9937762-A1.		
XX			
PD	29-JUL-1999.		
XX			
PF	02-DEC-1998; 98WO-EP07805.		
XX			
PR	09-OCT-1998; 98GB-0022135.		
PR	27-JAN-1998; 98EP-0300570.		
XX			
PA	(SMIK) SMITHKLINE BEECHAM PLC.		
XX			
PI	Chapman CG, Meadows HJ;		
XX			
DR	WPI; 1999-469126/39.		
DR	N-PSDB; Z00040.		
XX			
PT	New two pore potassium channel used for, e.g. treatment of cancer,		
PT	pulmonary, cardiovascular and inflammatory diseases		
XX			
PS	Claim 3; Page 26; 44pp; English.		
XX			
CC	This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1		
CC	polynucleotide Z00040. h-TREK1 is a two pore potassium channel.		
CC	The polynucleotide sequence of h-TREK1 can be used to diagnose a		
CC	disease or susceptibility to a disease related to expression or activ		
CC	of h-TREK-1 polypeptides. The methods of diagnosis may be used in the		
CC	treatment of diseases including cancer, pulmonary, cardiovascular, an		
CC	inflammatory diseases, pain, psychiatric disorders including depressi		
CC	and schizophrenia, neurodegenerative diseases including Alzheimer's,		
CC	stroke, and head trauma and neurological disorders including migraine		
XX			
SQ	Sequence 411 AA;		
Query Match	9.1%; Score 298.5; DB 20; Length 411;		
Best Local Similarity	28.5%; Pred. No. 3.5e-22;		
Matches	90; Conservative 64; Mismatches 121; Indels 41; Gaps		
QY	9 LLFTYISLMFGAAIYHHIEHGEEKISRAEORAKQAIANEYLLLEELGDKNTTODEILOR	68	

QY 288 TONRIWSG-----VTKDVG 301
 Db 278 -----wtgtvtarvtqrag 291

RESULT 9
 Y94426
 ID Y94426 standard; Protein; 393 AA.
 AC Y94426;

DT 04-AUG-2000 (first entry)
 DE Human h-TRAAK polypeptide #2.

Human; h-TRAAK: potassium channel polypeptide;
 2P domain potassium channel; neurodegenerative disease; stroke;
 psychiatric disorder; neurological disorder; Gene therapy.

OS Homo sapiens.
 PN WO200026253-A1.
 PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-GB03634.
 PR 03-NOV-1998; 98GB-0024048.
 PR 07-OCT-1999; 99GB-0023668.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Chapman CG, Duckworth DM;

DR WPI: 2000-365583/31.
 DR N-PSDB; A27106.

Novel isolated h-TRAAK polypeptides belonging to the potassium channel family of polypeptides, useful for the diagnosis and treatment of h-TRAAK related disorders, e.g. depression and schizophrenia

Claim 12; Pages 21 and 22; 35pp; English.

Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK polynucleotides from human tissue samples. h-TRAAK polypeptides have homology to the 2P domain potassium channel family of polypeptides. The h-TRAAK polypeptides and polynucleotides may be used in diagnostic assays for conditions related to h-TRAAK imbalance and for identifying agonists and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and polynucleotides may also be useful for treatment and prevention (e.g. as vaccines) of certain diseases, such as pain, psychiatric disorders including depression and schizophrenia, neurodegenerative disease including Alzheimer's, stroke and head trauma and neurological disorders including migraine and epilepsy. The present sequence is human h-TRAAK protein #2.

Sequence 393 AA;

Query Match 8.7%; Score 286; DB 21; Length 393;
 Best Local Similarity 27.9%; Pred. No. 6.4e-21;
 Matches 89; Conservative 57; Mismatches 115; Indels 58; Gaps 11;

QY 7 ILLLFYISYLMFGAAIYHTEHGPEKISRFAEQKRAQIAINEYLLEELGDKNTTQDEIL 66
 Db 7 lallalvilyvsqalvralteqpe-----qqaqrelgevreklfrhpcvdsqelg 59

QY 67 QRISDYCD-----KPVTLPTPTDPTWTFYHAFFFFAFTVCSVGVGNISPTTFAGRM 120
 Db 60 llikevadalgaggadpet-nstsnsshsawldgsaffsgtiittigynvalrtddarl 118

QY 121 IMIAYSVTIGIPVNGILFAGLGEYFGRT-----FEAYIRRYKKYKMTDMHYVPPQLGL 173

Db 119 fcifyalvgiplfgillagvgdrlgsslrhghieaiflk-----hvppeivr 168
 QY 174 ITTVVIALIPGIALFLVLPQCVGHLRELGLSSISLYSYVTTTIGFGDVPTFGANOP 233
 Db 169 vlsmalflligcllflvtptf-vfcymedwskleaiyfviutlttvgfgyva--gaopr 225
 QY 234 KEFGWFVVYQIFVIVWFIFSLGVLVIMTFTIRGLQ-----SKKLAYLEQQLSSNLKA 287
 Db 226 qd-----spayqplvwfwillglayfasvlttignwlrvsvrtraemggltaqaas---- 277
 QY 288 TONRIWSG-----VTKDVG 301
 Db 278 -----wtgtvtarvtqrag 291

RESULT 10

W23397

ID W23397 standard; Protein; 336 AA.

XX W23397;

DT 17-MAR-1998 (first entry)

DE TWIK-1 potassium channel protein.

KW TWIK-1 potassium channel; screening; diagnosis; transgenic animal;
 KW Tandem Of P domains in a Weak Inward rectifying K+; antibody.

OS Homo sapiens.

PN FR2744730-A1.

PD 14-AUG-1997.

PF 08-FEB-1996; 96FR-0001565.

PR 08-FEB-1996; 96FR-0001565.

PA (CNRS) CNRS CENT NAT RECH SCI.

PI Barhanin J, Duprat F, Fink M, Guillemare E, Lazdunski M;

PI Lesage F, Romey g;

XX WPI; 1997-427773/40.

XX N-PSDB; T64960;

XX Nucleic acid encoding new potassium channel designated TWIK-1 -
 PT useful for treating channel deficiency diseases, screening for
 PT active agents and for diagnosis

PS Claim 12; Figure 1b; 37pp; French.

XX The present sequence represents a protein comprising a potassium channel
 CC with the properties of a TWIK (Tandem of P domains in a weak inward
 CC rectifying K⁺)-1 channel. This is the first member of a new family of
 CC channels consisting of 4 transmembrane segments and two P domains, and
 CC being only weakly rectifying. The cDNA, vectors, the cells expressing
 CC TWIK-1 type channels and the protein are used to compensate
 CC for deficiency of potassium channels in various tissues. Compounds
 CC for modulating activity of TWIK-1 type channels may also be useful
 CC therapeutically, e.g. for control of epilepsy, arrhythmia, vascular
 CC disease, neurodegeneration (particularly of ischemic or anoxic origin),
 CC endocrine or muscular disorders. The cDNA and the vectors can also be
 CC used to create transgenic animals (especially knock-out animals) for use
 CC as models of TWIK-1 related diseases. Analysis of the sequence of the
 CC TWIK-1 gene may be used for pre-natal diagnosis of disease. Antibodies
 CC can be used to detect TWIK-1 channels and for inhibiting or activating
 CC the channels in vivo.

XX Sequence 336 AA;

XX SQ

```
Query Match 7.3%; Score 239; DB 18; Length 336;
Best Local Similarity 28.1%; Pred. No. 3.7e-16;
Matches 74; Conservative 49; Mismatches 112; Indels 28; Gaps 8;

QY 9 LLIFYSYLMFGAAIYVHIEGEEKISRABQKQAIAINEYLLLELGDKNNTTQDEILQR 68
Db 26 lvigyllylgavfsvsvelpyedllrqelrk----lkrflleehclseqqlqglgr 81
QY 69 ISYCDKPVTLPPYDDPTWTFYHAFFAFTVCSYGVGNISPTTFAGRMIMIAYSVI 128
Db 82 vleasnvgvsvlnasgn-wnwdfstalfastvltstgtyhtvpsdgkafciysvi 140
QY 129 GIPVNGILFAGLGEYFQRTFAYRYRYKYMSTDMHYVPPQLGL---ITTVVIALIPG- 184
Db 141 gipft-llf-----ltavvqrithvtrpvllyfhrwgfskqvvaivhavllgf 189
QY 185 --TALFLVLCVGHVHLRELGLSSISLYSYVTITGFGDYVPTFCANQPKFGGHVV 242
Db 190 vtscffifipaavfsvldedwnflesfycflstglgldgvyvpgyndk-----frel 244
QY 243 YQIFVIVWFISL-GYLVIMIMTF 264
Db 245 ykigitcylllgilamivletf 267

RESULT 11
Y87291
XX Y87291 standard; Protein; 394 AA.
AC Y87291;
XX
DT 11-MAY-2000 (first entry)
XX
DE Human signal peptide containing protein HSP-68 SEQ ID NO:68.
XX
KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; neuroprotection; neuroprotection; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's disease; ovulatory defect;
KW muscular dystrophy.
XX
OS Homo sapiens.
XX
XX WO200000610-A2.
XX
PD 06-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14484.
XX
PR 26-JUN-1998; 98US-0090762.
PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX
XX (INCY-) INCYTE PHARM INC.
XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
XX WPI: 2000-160673/14.
XX
DR N-PSDB; Z98176.
XX
XX New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
PS Claim 1; Page 207-208; 327pp; English.
XX
XX
```

```
CC 298109 to 298242 encode Y87224 to Y87357 which represent the human
CC signal peptide-containing proteins HSP-1 to HSP-134. HSPPs have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
CC or ribozyme therapeutics, for detecting related sequences or genetic
CC variations, and for chromosomal mapping. HSPP are also used to raise
CC specific antibodies (Ab) and to screen for agonists and antagonists
CC (potential therapeutic agents). Ab are used to diagnose, or monitor,
CC HSP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSP
CC from natural sources.
XX
SQ Sequence 394 AA;

Query Match 7.1%; Score 231.5; DB 21; Length 394;
Best Local Similarity 23.1%; Pred. No. 2.9e-15;
Matches 94; Conservative 76; Mismatches 150; Indels 87; Gaps 16;

QY 5 RWILLIFYSYLMFGAAIYVHIEGEEKIS-----RABQKQAIAINEYLLLELGDKN 58
Db 7 rtialivctfylvgaavfdalespelierqlrqlrarnysggvyeel---- 62
QY 59 TTTQDEILQISDYCDKPVTLPPYDDPTWTFYHAFFAFTVCSYGVGNISPTTFAG 118
Db 63 -----ervlrl-----kp-----hkagvqwrfgsfyfaictvittgghaapstdgg 106
QY 119 RMTIMAYSIVIGIPVNGILFAGLGEYFQRTFAYRYRYKYMSTDMHYVPPQLGL----I 174
Db 107 kvfcmyallgpltlvmfsgiserintivrylhrakk-----gigmradv 154
QY 175 TTVVIALIPGIALFLVLCVGHVHLR--ELGLSSISLYSYVTITGFGDYVPTFCANQ 232
Db 155 smanmvligffscistl-cigaaafshyehwtffqyyycfittltgfgdyv-aiqkdq 212
QY 233 PKFEGGWVYVYQIFVIVWFISLGYL--VNIMTFITRGLQSKKLAYLEQOL----- 281
Db 213 alqtqpqvafsfvyltltvlgafnlvrlfvtmnaedekrdehraltrngagg 272
QY 282 -----SSNLKATQNRNWSGVTKDVGYLRLRLNEL-YILKVPYVTDVDTAYTL 328
Db 273 gggggsahttdtasstaaagggrnrvyaevlhfgmcslwyksreklqys---ipmli 329
QY 329 PRSNCPLDLSMYRVEPAP-----IPSKRAFSVCADMVGAOREA 367
Db 330 prdlstdtcevqshspgggrysdtparr---clcs---gaprsa 370

RESULT 12
Y34132
ID Y34132 standard; Protein; 313 AA.
XX
AC Y34132;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human potassium channel K-Hnov49.
XX
KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW cardiovascular disorder; CNS disorder; renal disorder.
```


XX SQ Sequence 313 AA;

Query Match 6.4%; Score 210.5; DB 20; Length 313;
Best Local Similarity 24.5%; Pred. No. 3e-13;
Matches 70; Conservative 42; Mismatches 103; Indels 71; Gaps 9;

QY 10 LIFVSYLMFGAAIYHIEHGEKISRAEQKQAIAINEYLLLELGDKNKTTTODEILQRI 69
DB 11 laayaaylvlgallvarleghearirae-----le-----tlraqllqr- 50
QY 70 SDYCDKPVTLPPTYD-----DTPYTWTFYHAFFAFTVCS 104
DB 51 -----spcvaapaldafervlaagrlgrvvlanaasdpawdfasalfastlit 105
QY 105 TVGYGNISPTTFAGRMIMAYSIGIPVNGILFAGLGEYFGRTFEAIYRKYKMKSTDM 164
DB 106 tvgygytptldagkafsaifallgvpttmllltasaqrslslthvplswlsmrgwdp 165
QY 165 H-----YVPPQLGLITTVVIALIPGIALFLVPCVGHLLRELGLSSISLYSYVVTMTTI 219
DB 166 rraacwhlvallgvvtv-----cfllpavifah-leeawsfldafyfcfislsti 215
QY 220 GFQGYVPTFGANQPKFGGWFVYQIFVIVWFIFSLGYLVMM-TF 264
DB 216 glgdyvpgaeagqp-----yralykvltvtyflglvamlvltqtf 256

RESULT 14
Y68737
ID Y68737 standard; Protein; 313 AA.
AC Y68737;
XX
XX
DT 05-MAY-2000 (first entry)
XX
DE KT4, a TWIK family 2PD potassium channel polypeptide.
XX
XX KT4; TWIK family 2PD potassium channel polypeptide; P-domain;
KW expressed sequence tag; EST; AA604914; ion channel dysfunction;
KW renal disease; musculoskeletal disease; proliferative disease;
KW renal failure; nephrosis; cirrhosis; dysphagia; gastritis; myotonia;
KW muscular dystrophy; atherosclerosis; cancer.
XX
OS Homo sapiens.
XX
XX WO200003687-A2.
XX
XX 27-JAN-2000.
XX
XX 20-JUL-1999; 99WO-US16471.
XX
XX 20-JUL-1998; 98US-0093486.
XX
XX 13-AUG-1998; 98US-0096655.
XX
XX (ELAN-) ELAN PHARM INC.
XX
XX Forsayeth JR, Zhao BB, Chavez RA;
XX
XX WPI; 2000-171196/15.
XX
XX N-PSDB; 246092.
XX
XX Novel human potassium channel polynucleotides and polypeptides used in
PT the diagnosis, prevention and treatment of diseases including renal
PT failure, cirrhosis, muscular dystrophy and cancers -
XX
XX Claim 4; Fig 1A-C; 53pp; English.
XX
XX The present sequence represents a protein, designated KT4, which is a
CC member of the TWIK family 2PD potassium channel polypeptides. These
CC polypeptides contain two potential P-domains and 8 (preferably 4)
CC transmembrane domains. The KT4 cDNA sequence was isolated from a brain

CC cDNA library using degenerate oligonucleotides derived from human
CC expressed sequence tag (EST) AA604914. The polypeptides and
CC polynucleotides are used in the diagnosis, prevention and treatment of
CC disease states. The polynucleotides may be used to detect and
CC quantitate expression of TWIK family 2PD potassium channels, and
CC aberrant or mutant forms of the polynucleotide which cause various
CC diseases and disorders. Antisense oligonucleotides may be used to
CC modulate the expression of polynucleotides of the invention. The
CC polypeptides are used for treating diseases and disorders associated
CC with ion channel dysfunction, including renal, musculoskeletal and
CC proliferative diseases, e.g. renal failure, nephrosis, cirrhosis,
CC dysphagia, gastritis, myotonias, muscular dystrophy, atherosclerosis
XX and cancers.
XX
XX Sequence 313 AA;

Query Match 6.4%; Score 210.5; DB 21; Length 313;
Best Local Similarity 24.5%; Pred. No. 3e-13;
Matches 70; Conservative 42; Mismatches 103; Indels 71; Gaps 9;

QY 10 LIFVSYLMFGAAIYHIEHGEKISRAEQKQAIAINEYLLLELGDKNKTTTODEILQRI 69
DB 11 laayaaylvlgallvarleghearirae-----le-----tlraqllqr- 50
QY 70 SDYCDKPVTLPPTYD-----DTPYTWTFYHAFFAFTVCS 104
DB 51 -----spcvaapaldafervlaagrlgrvvlanaasdpawdfasalfastlit 105
QY 105 TVGYGNISPTTFAGRMIMAYSIGIPVNGILFAGLGEYFGRTFEAIYRKYKMKSTDM 164
DB 106 tvgygytptldagkafsaifallgvpttmllltasaqrslslthvplswlsmrgwdp 165
QY 165 H-----YVPPQLGLITTVVIALIPGIALFLVPCVGHLLRELGLSSISLYSYVVTMTTI 219
DB 166 rraacwhlvallgvvtv-----cfllpavifah-leeawsfldafyfcfislsti 215
QY 220 GFQGYVPTFGANQPKFGGWFVYQIFVIVWFIFSLGYLVMM-TF 264
DB 216 glgdyvpgaeagqp-----yralykvltvtyflglvamlvltqtf 256

RESULT 15
Y68738
ID Y68738 standard; Protein; 313 AA.
AC Y68738;
XX
XX
DT 05-MAY-2000 (first entry)
XX
DE KT5, a TWIK family 2PD potassium channel polypeptide.
XX
XX KT5; TWIK family 2PD potassium channel polypeptide; P-domain;
KW expressed sequence tag; EST; AA533124; ion channel dysfunction;
KW renal disease; musculoskeletal disease; proliferative disease;
KW renal failure; nephrosis; cirrhosis; dysphagia; gastritis; myotonia;
KW muscular dystrophy; atherosclerosis; cancer.
XX
XX Homo sapiens.
XX
XX WO200003687-A2.
XX
XX 27-JAN-2000.
XX
XX 20-JUL-1999; 99WO-US16471.
XX
XX 20-JUL-1998; 98US-0093486.
XX
XX 13-AUG-1998; 98US-0096655.
XX
XX (ELAN-) ELAN PHARM INC.
XX
XX Forsayeth JR, Zhao BB, Chavez RA;
XX
XX

```
DR WPI: 2000-171196/15.
DR N-PSDB: 246094.
XX
PT Novel human potassium channel polynucleotides and polypeptides used in
PT the diagnosis, prevention and treatment of diseases including renal
PT failure, cirrhosis, muscular dystrophy and cancers -
XX
PS Claim 7; Fig 3A-C; 53pp; English.
XX
CC The present sequence represents a protein, designated KT5, which is a
CC member of the TWIK family 2PD potassium channel polypeptides. These
CC polypeptides contain two potential P-domains and 8 (preferably 4)
CC transmembrane domains. The KT4 cDNA sequence was isolated from a brain
CC cDNA library using degenerate oligonucleotides derived from human
CC expressed sequence tag (EST) AA533124. The polypeptides and
CC polynucleotides are used in the diagnosis, prevention and treatment of
CC disease states. The polynucleotides may be used to detect and
CC quantitate expression of TWIK family 2PD potassium channels, and
CC aberrant or mutant forms of the polynucleotide which cause various
CC diseases and disorders. Antisense oligonucleotides may be used to
CC modulate the expression of polynucleotides of the invention. The
CC polypeptides are used for treating diseases and disorders associated
CC with ion channel dysfunction, including renal, musculoskeletal and
CC proliferative diseases, e.g. renal failure, nephrosis, cirrhosis,
CC dysphagia, gastritis, myotonias, muscular dystrophy, atherosclerosis
CC and cancers.
XX
SQ Sequence 313 AA;

Query Match 6.4%; Score 210.5; DB 21; Length 313;
Best Local Similarity 24.5%; Pred. No. 3e-13;
Matches 70; Conservative 42; Mismatches 103; Indels 71; Gaps 9;

Oy 10 LIFYSYLMFGAAIYHIEHGEKISRAEQKQAIATNEYLLEELGDKNTTQDEILORI 69
Db | | :||: || : :| | ||| | | : :|||
Oy 11 laayaaylvlgallvarlegphearlae-----le-----tlraqllgr- 50
Db | | :||: || : :| | ||| | | : :|||
Oy 70 SDYCDKPVTLPTYP-----DTPYTWTFYHAFFFAFTVCS 104
Db | | :||: || : :| | ||| | | : :|||
Oy 51 -----spcvaapaldafervvlaagrlgrvvlanasgsanasdpawdfasalfastlit 105
Db | | :||: || : :| | ||| | | : :|||
Oy 105 TVGYNISPTTFAGRMIMAYSVIGIPVNGILFAGLGEYFGTFFAIYRRYKXKXMTDM 164
Db | | :||: || : :| | ||| | | : :|||
Oy 106 tvgygyttpltdagkafsfafallgvpttmllltasagrlslthvplswlsmrwgwdp 165
Db | | :||: || : :| | ||| | | : :|||
Oy 165 H-----YVPPOLGLTTVVIALPGIALFLPVCVGHLLRELGLSSLSLYSVYVTTTI 219
Db | | :||: || : :| | ||| | | : :|||
Oy 166 rraacwhivallgvvvtv-----cflvpavifah-leeawfldafyfcfislsti 215
Db | | :||: || : :| | ||| | | : :|||
Oy 220 GFGDYVPTFGANQPKFEGGVFVYQIFVWVFISLGYLVMMIM-TF 264
Db | | :||: || : :| | ||| | | : :|||
Oy 216 glgdyvpgeapqp-----yralykvltvylfglvamlvvlqltf 256
Db | | :||: || : :| | ||| | | : :|||
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 17, 2001, 19:24:58 ; Search time 65.58 Seconds
(without alignments)
169.220 Million cell updates/sec

Title: US-08-816-011C-2

Perfect score: 3283

Sequence: 1 MSPNRWILLIFYISYLMFG.....DAVRHPSNRMAWPAAG 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6-COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3283	100.0	618	1	US-08-332-312-2
2	239	7.3	336	3	US-08-749-816-2
3	204.5	6.2	336	1	US-08-332-312-4
4	189	5.8	383	3	US-08-749-816-4
5	165.5	5.0	347	3	US-08-749-816-3
6	116.5	3.5	888	2	US-08-956-242-4
7	116.5	3.5	888	3	US-09-351-215-4
8	110.5	3.4	2465	2	US-08-596-291-3
9	110.5	3.4	2465	3	US-09-100-804-3
10	110.5	3.4	2466	3	US-09-080-855-12
11	110.5	3.4	2466	4	PCT-US94-09943-2
12	101.5	3.1	390	2	US-08-614-156B-3
13	100.5	3.1	390	2	US-08-614-156B-1
14	100	3.0	1754	1	US-07-745-206A-13
15	100	3.0	1754	2	US-08-311-363-13
16	97.5	3.0	581	3	US-09-135-021-80
17	97.5	3.0	676	3	US-09-135-021-2
18	93.5	2.8	434	3	US-08-725-459B-42
19	93	2.8	770	1	US-08-445-135-2
20	92	2.8	3169	2	US-08-477-451-6
21	89	2.7	1159	2	US-08-956-242-13
22	89	2.7	1159	3	US-09-351-215-13
23	88.5	2.7	626	2	US-08-956-242-2
24	88.5	2.7	626	3	US-09-351-215-2
25	88.5	2.7	1481	2	US-08-616-844-40
26	88.5	2.7	1481	2	US-08-599-654-40
27	88.5	2.7	1481	3	US-08-944-868A-40
28	88.5	2.7	1481	3	US-08-944-423A-40

29 88.5 2.7 1481 3 US-08-944-496-40 Sequence 40, Appli
30 88.5 2.7 2289 3 US-09-051-019-2 Sequence 2, Appli
31 88 2.7 369 2 US-08-424-224-2 Sequence 2, Appli
32 88 2.7 369 4 PCT-US94-02891-69 Sequence 69, Appli
33 87.5 2.7 1503 3 US-08-976-255-14 Sequence 14, Appli
34 86.5 2.6 424 2 US-08-614-155B-1 Sequence 1, Appli
35 86.5 2.6 424 2 US-08-614-155B-3 Sequence 3, Appli
36 86.5 2.6 532 1 US-08-288-405A-10 Sequence 10, Appli
37 86.5 2.6 557 1 US-08-424-788-6 Sequence 5, Appli
38 86.5 2.6 578 1 US-08-424-788-5 Sequence 5, Appli
39 86.5 2.6 578 1 US-08-110-683-2 Sequence 2, Appli
40 86.5 2.6 578 2 US-08-683-743-2 Sequence 2, Appli
41 86.5 2.6 578 2 US-08-477-166-2 Sequence 2, Appli
42 86.5 2.6 578 2 US-08-472-097-2 Sequence 2, Appli
43 86.5 2.6 578 4 PCT-US93-11638-2 Sequence 2, Appli
44 86.5 2.6 1969 3 US-08-836-325-16 Sequence 16, Appli
45 86 2.6 902 1 US-08-396-479B-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-08-332-312-2

; Sequence 2, Application US/08332312

; Patent No. 5559026

; GENERAL INFORMATION:

; APPLICANT: Price, Laura A.

; APPLICANT: Pausch, Mark H.

; TITLE OF INVENTION: Functional Expression of a Drosophila

; TITLE OF INVENTION: Melanogaster Putative Potassium Channel in Yeast

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: US

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/332,312

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Harrington, James J.

; REGISTRATION NUMBER: P-38,711

; REFERENCE/DOCKET NUMBER: 32,421

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-831-3246

; TELEFAX: 201-831-3305

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 618 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-332-312-2

Query Match 100.0%; Score 3283; DB 1; Length 618;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSPNRWILLIFYISYLMFGAIIYVHIEGEEKISRAEQKAOIAINEYLLLELGDKNNT 60

|||||

Db 1 MSPNRWILLIFYISYLMFGAIIYVHIEGEEKISRAEQKAOIAINEYLLLELGDKNNT 60

|||||

Oy 61 TQDEILQRISDYCDKPVTLPTTYDDTYTWTFFHAFFAFTVCSTVGXGNISPTTFAGRM 120

Db 61 TQBEILQRIQSDYCKPVTLPPTDPTTFTYHAEFFAFVTCSTVGYNISPTTFAGRM 120
QY 121 IMIAYSIGIPVNGILFAGLGEYFGRTFEALYRKYKMYKSTDMHYVPPQGLITTVIA 180
Db 121 IMIAYSIGIPVNGILFAGLGEYFGRTFEALYRKYKMYKSTDMHYVPPQGLITTVIA 180
QY 181 LIPGIALFLVPCGVHLLRELGLSSISLYSVVTTTIGFGDYVPTFGANQKKEGGWF 240
Db 181 LIPGIALFLVPCGVHLLRELGLSSISLYSVVTTTIGFGDYVPTFGANQKKEGGWF 240
QY 241 VYQIFVIVWFIFSLGYLWIMTFITRGLQSKKLAYLEQQLSSNLKATQNRWSGVTKDV 300
Db 241 VYQIFVIVWFIFSLGYLWIMTFITRGLQSKKLAYLEQQLSSNLKATQNRWSGVTKDV 300
QY 301 GYLRRMLNELYLKVPVYTDVIAITLPRNSNCPDLMSYRVEPAPIPSRKRAFSVCADM 360
Db 301 GYLRRMLNELYLKVPVYTDVIAITLPRNSNCPDLMSYRVEPAPIPSRKRAFSVCADM 360
QY 361 VQAQREAGMVFHANSDDTLKLDREKTFETAAYHQTDLAKVYNALATVKPPPAEQEDA 420
Db 361 VQAQREAGMVFHANSDDTLKLDREKTFETAAYHQTDLAKVYNALATVKPPPAEQEDA 420
QY 421 ALYGGYHGFSDSILASEWSFSTVNEFTSPRRPRARACSDFNLEAPRWQSERPLRSRSHNE 480
Db 421 ALYGGYHGFSDSILASEWSFSTVNEFTSPRRPRARACSDFNLEAPRWQSERPLRSRSHNE 480
QY 481 WTWSGDNQIQEAFNORYKQOQANGAANSTWVHLPEALDEEOLRNHRVPVARSPPCR 540
Db 481 WTWSGDNQIQEAFNORYKQOQANGAANSTWVHLPEALDEEOLRNHRVPVARSPPCR 540
QY 541 MVDVCFPPSRRTPRRIWASCPWSRYPRVSSRRKPDPRWTTTSTRSRPPVPNPICATDA 600
Db 541 MVDVCFPPSRRTPRRIWASCPWSRYPRVSSRRKPDPRWTTTSTRSRPPVPNPICATDA 600
QY 601 VRURPSNRMAWPAAGAAG 618
Db 601 VRURPSNRMAWPAAGAAG 618

RESULT 2
US-08-749-816-2
; Sequence 2, Application US/08749816
; Patent No. 6013470
; GENERAL INFORMATION:
; APPLICANT: Lesage, Florian
; APPLICANT: Guillemate, Eric
; APPLICANT: Fink, Michel
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lazdunki, Michel
; APPLICANT: Romey, Georges
; APPLICANT: Barhanin, Jacques
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
; TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
; TITLE OF INVENTION: OF DRUGS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,816
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: P-38,711
; REFERENCE/DOCKET NUMBER: 32,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305

; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989,6351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8393
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-749-816-2

Query Match 7.3%; Score 239; DB 3; Length 336;
Best Local Similarity 28.1%; Pred. No. 8.7e-17;
Matches 74; Conservative 49; Mismatches 112; Indels 28; Gaps 8;

QY 9 LLIFFIYSLMFGAAIYYHIEHGEKISRRAQKAIQAINELLEEGLDKNTTTQDEILQR 68
Db 26 LVLGYLLLVFAGAVFSSVPELVEDLLRQELRK----LKRFLLEEHECLSEQOLEQFLGR 81
QY 69 ISDYCDKPVLPPTYDDTPTTYTFFHAFFAFTVCSVTGYGNTSPPTFAGRMIMIAYSVI 128
Db 82 VLEASNYGVSVLSNASGN-WNWDFTSALFFASTVLTSTGYGTVPLSDGGKAFCAIYSVI 140
QY 129 GIPVNGILFAGLGEYFGRTFEALYRKYKMYKSTDMHYVPPQGL---ITTVVIALIPG- 184
Db 141 GIPFT-LLF-----LTAVQRTVHVRPRVLYFHIRMGFSKQVVAIVHAVLLGF 189
QY 185 --IALFLVPCGVHLLRELGLSSISLYSVVTTTIGFGDYVPTFGANQKKEGGWFV 242
Db 190 VIVSCFFIPAAVSVLEDDWNFLESFYCFISLSIGLDYVPGEGYNQK-----FREL 244
QY 243 YQIFVIVWFIFSL-GYLVIMTF 264
Db 245 YKIGITCYLLGLLIAMLVVLETF 267

RESULT 3
US-08-332-312-4
; Sequence 4, Application US/08332312
; Patent No. 5559026
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; APPLICANT: Pausch, Mark H.
; TITLE OF INVENTION: Functional Expression of a Drosophila
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,312
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: P-38,711
; REFERENCE/DOCKET NUMBER: 32,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305


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; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Welser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989,6351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-749-816-3

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Query Match 5.0%; Score 165.5; DB 3; Length 347;
Best Local Similarity 25.0%; Pred. NO. 5.5e-09;
Matches 78; Conservative 38; Mismatches 109; Indels 87; Gaps 12;

Qy	1	MSPN-----RWILLIFYISYLMF---GAAYIYHHIEHGEEKISRAEPQKAAQIAINE	48
Db	22	MSPTNRQFRQNQNVVNVVSAATLLVFNLIAGAGIFY-----LAETQNSSESLNE	71
Qy	49	YLLEELGDKNTTTODEILORISYCDKQVTLPTTYDDTPVTMTFYHAFFFAFTVCSTGV	108
Db	72	NSEVSKCLHNLPIGGKLTAEKMSKLGCKLTKSSRIDG-----FGKAIIFSWTLISTVGY	125
Qy	109	GNISPTTFACRMTMIAYSIGVIGIPVNGILFAGLGEYFG-----RTPEAIYVRVK	156
Db	126	GSYPHSTLGRYLTIFYSLMIPV---FIAKFEFGTFLAHFLVYVVSNRTRLAVKAKAY	181
Qy	157	KYKMSDTHMVVPQO-----LGLITTVVIALIGIALFLVLPQVGHLLRELGLSST	207
Db	182	KLSONPENAETPSNSLQHDYLIPLSULLCSISLLSSSALFSSNIISY-----LSSV	234
Qy	208	SLYYSVYTTTTIGFDYVYTFPGANQPKFEGGWVYVQIFVYVWFISLGLVNIWMTFITR	267
Db	235	--YFGIITMFLIGIDIVPT-----NLVWF---SGY---CMFLIS	267
Qy	268	GLQSKKLAYLEQ	279
Db	268	DVLSNOIFYFCO	279

RESULT	6
US-08-956-242-4	
: Sequence 4, Application US/08956242C	
: Patent No. 5986081	
: GENERAL INFORMATION:	
: APPLICANT: Ganetzky, Barry S.	
: APPLICANT: Titus, Steven A.	
: TITLE OF INVENTION: Polynucleotides Encoding Herg-3	
: FILE REFERENCE: 960296.94550	
: CURRENT APPLICATION NUMBER: US/08/956,242C	
: CURRENT FILING DATE: 1997-10-22	
: NUMBER OF SEQ ID NOS: 13	
: SOFTWARE: PatentIn Ver. 2.0	
: SEQ ID NO 4	
: LENGTH: 888	
: TYPE: PRT	
: ORGANISM: Homo sapien	
: FEATURE:	
: NAME/KEY: unsure	
: LOCATION: (133)	
: OTHER INFORMATION: Unidentified at time of filing	
: FEATURE:	
: NAME/KEY: unsure	
: LOCATION: (181)	
: OTHER INFORMATION: Unidentified at time of filing	
: FEATURE:	
: NAME/KEY: unsure	
: LOCATION: (181)	
: OTHER INFORMATION: Unidentified at time of filing	
: FEATURE:	
: NAME/KEY: unsure	
: LOCATION: (610)	
: OTHER INFORMATION: Unidentified at time of filing	
: FEATURE:	
: NAME/KEY: unsure	
: LOCATION: (611)	
: OTHER INFORMATION: Unidentified at time of filing	
: FEATURE:	
: NAME/KEY: unsure	
: LOCATION: (621)	
: OTHER INFORMATION: Unidentified at time of filing	
: FEATURE:	
: NAME/KEY: unsure	
: LOCATION: (624)	
: OTHER INFORMATION: Unidentified at time of filing	
: FEATURE:	
: NAME/KEY: unsure	
: LOCATION: (625)	
: OTHER INFORMATION: Unidentified at time of filing	
: FEATURE:	
: NAME/KEY: unsure	
: LOCATION: (628)	
: OTHER INFORMATION: Unidentified at time of filing	
: FEATURE:	


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Best Local Similarity   20.3%; Pred. No. 0.095;
Matches    66; Conservative     52; Mismatches   118; Indels      89; Gaps       13

QY 263 TFIPTGLOSGLAYLEQQQLSSNLKATONRWISGVTKDVGYLRLMLNE-----SNDNYFKDIILSDNSGREDSNTFCP 309
Db 231 TLNKLGL-SKSMGF-----SIKDQT-----DKDTQ-----DNFYKDIILSDNSGREDSNTFCP 274

QY 310 -----LYLKYKPVY-TDVADIATPLPRSNCPDLMSMYR-----VEPA 345
Db 275 YQFXTSGPEKKPIFGIDVLSSKKKIWASSMDLLCTADRDFFSGSETATYRRCHPEAVTVRTS 334

QY 346 PIPSEKRA----PSVCADMCAQREAGMVHANSOTIDLTKLDREKTFTAEAYHQTTDLLA 401
Db 335 TTTPRKKEARYSGDSTALDFPGPKMDPIYHT-----RELPTSSAILSSALDRIR 382

QY 402 KVNVALATVPKPPAEQEADAALYGCVHG--FSDS-----OILASEWSFSTVNETSPRRRPRA 455
Db 383 ERQKKLOVLRAMNVEEPVRYKYKHGGVDVFSTSSSEPSIIISE-----SDPROVRSEA 436

QY 456 RACSDFNLEAP-----RWOSERPLRSNHNEWTSWGDNQIQEAFNQRYKGQQQRANGAA 508
Db 437 SKRPESSSLPGVDETLSOGQSQRPSRQYETPFEGNLINQEIIMLKROEELMQLQAKMAL 496

QY 509 NSTWVHLEP-DALEEOLRNHRVPV 532
Db 497 QSRSLSLYPGDTIKASMLDITRDEL 521

RESULT          9
US-09-100-804-3
: Sequence 3, Application US/09100804
: Patent No. 6066472
: GENERAL INFORMATION:
: APPLICANT: GONEZ, LEONEL JORGE
: APPLICANT: SARAS, JAN
: APPLICANT: CLAESSEN-WELSH, LENA
: TITLE OF INVENTION: HELDIN, CARL-HENRIK
: TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
: TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
: TITLE OF INVENTION: TYROSINE PHOSPHATASES
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
: STREET: 600 ATLANTIC AVENUE
: CITY: BOSTON
: STATE: MASSACHUSETTS
: COUNTRY: USA
: ZIP: 02210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/100,804
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/596,291
: FILING DATE: 09-AUG-1996
: APPLICATION NUMBER: US 08/115,573
: FILING DATE: 01-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/09943
: FILING DATE: 01-SEP-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: GATES, EDWARD R.
: REGISTRATION NUMBER: 31,616
: REFERENCE/DOCKET NUMBER: LO461/7003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-720-3500
: TELEFAX: 617-720-2441
: TELEX:

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-100-804-3

Query Match          3.4%;   Score 110.5;   DB 3;   Length 2465;
Best Local Similarity 20.3%;   Pred. No. 0.095;
Matches 66;   Conservative 52;   Mismatches 118;   Indels 89;   Gaps

Qy 263 TFITRGLQSKKLAYLEOQLSSNLKATQNRILWSGVTKDVGYLRLMNE-----309
Db 231 TFLNKL-SKSMGFL-----SIKDTQ-----DENYFKDILSDNSGREDSSENTFCP 274

Qy 310 -----LYILVKVPVY-TDVDIATLPRNSCPDLSMYR-----VEPA 345
Db 275 YQFKTSGPEKKPIGIDVLSSKKKIWASSMDLLCTADRFSSGETATYRRCHPEAVTVRTS 334

Qy 346 PIPSRKRA---EVSVCADMYGAQREAGVGHANSDDTLTKLDREKTFETAAYHQTTDLIA 401
Db 335 TTPRKKKARYSDGSIALDIFGPKMDPIYHT-----RELPTSSAIISSALDRIR 382

Qy 402 KVVNALATVPKPPAEQDDAALYGGYHG--FSDS---QILASEWSFSTWNETSPRRPRA 455
Db 383 ERQKKLQVLRAMNVPEPVRYKYTHGVFESTSESPSIISE-----SDFOYVRSEA 436

Qy 456 RACSDFNLEAP-----RWOSRPLRSSHNWTSGDNOQIQEAFNQRYKQOQRANGAA 508
Db 437 SKRPESSSGLPGVDETLSQGSQSRPSQRYETPTEGNNLQEIIMLKROEELMLOAKMAL 496

Qy 509 NSTMVHLEP-DALEEQLRNHRVPV 532
Db 497 QSRLSLYPGDTIKASMLDITRDPL 521

RESULT 10
US-09-080-855-12
; Sequence 12, Application US/09080855A
; Patent No. 6083721
; GENERAL INFORMATION:
; APPLICANT: Saras, Jan
; APPLICANT: Franzn, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Olf
; APPLICANT: Gonez, Leonel Jorge
; APPLICANT: Heidln, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS W
; FILE REFERENCE: I0461/7030
; CURRENT APPLICATION NUMBER: US/09/080,855A
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: 08/805,583
; EARLIER FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-080-855-12

Query Match          3.4%;   Score 110.5;   DB 3;   Length 2466;
Best Local Similarity 20.3%;   Pred. No. 0.095;
Matches 66;   Conservative 52;   Mismatches 118;   Indels 89;   Gaps

Qy 263 TFITRGLQSKKLAYLEOQLSSNLKATQNRILWSGVTKDVGYLRLMNE-----309
Db 231 TFLNKL-SKSMGFL-----SIKDTQ-----DENYFKDILSDNSGREDSSENTFCP 274

Qy 310 -----LYILVKVPVY-TDVDIATLPRNSCPDLSMYR-----VEPA 345

```

```

Query Match          3.4%; Score 110.5; DB 3; Length 2466;
Best Local Similarity 20.3%; Pred. No. 0.095;
Matches 66; Conservative 52; Mismatches 118; Indels 89; Gaps 13;

Qy 263  TTITRGLOSKLAYLEQOLSSNLKATONRIWSGVTKDGYLRRLNE----- 309
      ||| :|| ||| :|
Db 231  TFLNKGKL-SKSMGEL-----SIRDTQ-----DENYFKDILSONSGREDSENTFSP 274

Qy 310  LYLILKVKPVY--TDVDIAYTLPRNSCPDILSMYK-----VEPA 345

```

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Db      275 YQKTSGEKKPIPGIDVLSKKKIWASSMDLLCTADRFSSGSETATVRCHPEAVTVRTS   334  
       : : | : | : | : | : | : | : | : | : | : | : | : |  
  
Qy     346 PIPSRKRA-----FSVCADMVGQAOREAGMVHANSDDTLTKLDREKTFTETAAYHOTDILLA 401  
       : : | : | : | : | : | : | : | : | : | : | : | : |  
Db     335 TTPRKKEARYSGSIALDFGPKQWDPIYHT-----RELPTSSAISALDRIR    382  
       : : | : | : | : | : | : | : | : | : | : | : | : |  
  
Qy     402 KVNVALATVKPPPAEQEDDAALYGGHG----FSDS-----OILASEWSFSTNVNFTSPRRPRA 455  
       : : | : | : | : | : | : | : | : | : | : | : | : |  
Db     383 ERQKQLQVLREAANVEEPVRYRKYTHGVGFSTSSEPSIIISSE-----SDFROVRRSEA 436  
       : : | : | : | : | : | : | : | : | : | : | : | : |  
  
Qy     456 RACSDENLEAP-----RWQSERPLRSNSHNETHSWGDNQQIQEAFNQRYKGQORANGAA 508  
       : : | : | : | : | : | : | : | : | : | : | : | : |  
Db     437 SKFESSGLPVGDETLQSQRQRSFYETPFEGNLINQEIMLKROEEELMLQAKMAL 496  
       : : | : | : | : | : | : | : | : | : | : | : | : |  
Qy     509 NSTMWHLEP-DALEEQLRNHRVPV 532  
       : : | : | : | : | : | : | : | : | : | : | : | : |  
Db     497 RQSRLSLPGDTIKASMLDIITRDPL 521  
       : : | : | : | : | : | : | : | : | : | : | : | : |  
  
RESULT 11  
PCT-US94-09943-2  
; Sequence 2, Application PC/TUS9409943  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; APPLICANT:  
; APPLICANT:  
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; STREET: 600 ATLANTIC AVENUE  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/U94/09943  
; FILING DATE: 01-SEP-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/115,573  
; FILING DATE: 01-Sep-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TWOMEY, MICHAEL J.  
; REGISTRATION NUMBER: P-38,349  
; REFERENCE/DOCKET NUMBER: L0461/7000WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/720-3500  
; TELEX: 617/720-2441  
; TELEFAX: 92-1742 EZEKIEL  
; INFORMATION FOR SEQ ID NO.: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2466 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US94-09943-2
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Query Match      3.4%; Score 110.5; DB 4; Length 2466;
Best Local Similarity 20.3%; Pred. No. 0.095;
Matches 66; Conservative 52; Mismatches 118; Indels 89; Gaps 13;

QY 263 TTTTGTGQSCKKLAYLEOOLSSNLKATONIGSWGTVKDGYLRRLMNE----- 309
||| : || | : | : ||| | : | : |
```

```

Db 231 TFLNGL-SKSMGL-----SIKDT-----DENYFKDILSDNSGREDSNTFSP 274
Qy 310 -----LVILKVPY-TVDIATYLPNSNCPDLSMYR-----VEPA 345
Db 275 YQFTSGPEKKPIGIDVLKKKIIWASSMDLLCTADRFSSGETATYRRCHPEAVTVRTS 334
Qy 346 PIPSRKA-----FSVCADMYGAQREAGMVHANSDTDLTKLDREKTFETAAYHQTTDLA 401
Db 335 TTPRKKKARYSDGSIAUDIFGPKMDPIYHT-----RELPTSAISSALDRIR 382
Qy 402 KVWALATVAPPPAEQEDAAALGYGHC--FSDS-----QILASEWSFSTVNETSPRRPRA 455
Db 383 ERQKKLOVLEAMNVEPVRYKTYHGVFSTSESPTSISSE-----SDFQVRSER 436
Qy 456 RACSDFNLEAP-----RWQSRPLRSSHNWTWGDNQIOEAFNQRYKGOORANGAA 508
Db 437 SKRFESSGLPGVDETLSQGSORSPRQYETTFEGNLINQEIIMLKQEEELMQLAKMAL 496
Qy 509 NSTMVHLEP-DALEEQLRNHRHPV 523
Db 497 QSRLSLYPGDTIKASMLDITRDPL 521

RESULT 12
us-08-614-156B-3
; Sequence 3, Application us/08614156B
; Patent No. 5917027
; GENERAL INFORMATION:
; APPLICANT: Susumu SETNO et al.
; TITLE OF INVENTION: NOVEL ATP-SENSITIVE POTASSIUM-CHANNEL
; TITLE OF INVENTION: PROTEINS AND THEIR GENES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC
; STREET: 400 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614,156B
; FILING DATE: 12-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 264943/1995
; FILING DATE: 18-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PLAYER, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10890/P60282US0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-638-6666
; TELEFAX: 202-393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-614-156B-3

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Query Match 3.1%; Score 101.5; DB 2; Length 390;
Best Local Similarity 26.3%; Pred. No. 0.039;
Matches 45; Conservative 27; Mismatches 56; Indels 43; Gaps 7;
QY 91 TTFYHAFFAFTVCTGVGNGISPTTFAGRM-----IMIAYSVIGIPVNGILFAGL 140

Db 116 SFSSAFLEIEVQVTIGFG-----GRMTEECPLAILIVQNVGLMINAIM---L 164
Qy 141 GEYGRTEAIEYRYKKYKMDHMYVPPQLGITVVVIALIPGIALFLVLPVCGVHLLR 200
Db 165 GCIEFMKTAQA-HRRAETLIFSKH-----AVITLRHGRLCFM---LRVGDRL 206
Qy 201 ELGLSSISLYSYVTTTIGFDYVPTFGANQPKFEG-----GWFFVYQIFV 247
Db 207 KSMIISATIHQVVRKTTSPGEVYVPLHQVDIPMENGVGNGIPLVAPLII 257

RESULT 13

US-08-614-156B-1
; Sequence 1, Application US/08614156B
; Patent No. 5917027
; GENERAL INFORMATION:
; APPLICANT: Susumu SEINO et al.
; TITLE OF INVENTION: NOVEL ATP-SENSITIVE POTASSIUM-CHANNEL
; TITLE OF INVENTION: PROTEINS AND THEIR GENES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC
; STREET: 400 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614.156B
; FILING DATE: 12-MAR-1996
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 264943/1995
; FILING DATE: 18-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PLAYER, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10890/P60282US0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-638-6666
; TELEFAX: 202-393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-614-156B-1
Query Match 3.1%; Score 100.5; DB 2; Length 390;
Best Local Similarity 26.8%; Pred. No. 0.05;
Matches 42; Conservative 25; Mismatches 51; Indels 39; Gaps 6;

Qy 91 TTYHAFFAFTVCSYGVGNISPTTFAGRM-----MIAYSVIGIPVNGILFAGL 140
Db 116 SFSSAFLEIEVQVTIGFG-----GRMTEECPLAILIVQNVGLMINAIM---L 164
Qy 141 GEYGRTEAIEYRYKKYKMDHMYVPPQLGITVVVIALIPGIALFLVLPVCGVHLLR 200
Db 165 GCIEFMKTAQA-HRRAETLIFSKH-----AVITLRHGRLCFM---LRVGDRL 206

Qy 201 ELGLSSISLYSYVTTTIGFDYVPTFGANQPKFEG 237
Db 207 KSMIISATIHQVVRKTTSPGEVYVPLHQVDIPMENG 243

RESULT 14

US-07-745-206A-13
; Sequence 13, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Feldman, Daniel

; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods

; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/745.206A
; FILING DATE: 19910815
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1754 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-745-206A-13

Query Match 3.0%; Score 100; DB 1; Length 1754;
Best Local Similarity 21.2%; Pred. No. 0.69;
Matches 121; Conservative 69; Mismatches 184; Indels 196; Gaps 34;

Qy 120 MIMTAYSVIGIPVNGILFAG-----LGEYFG---RTFEAYRYRYKKYKM 160
Db 1276 LFMFIFAVIAVQ---LFGKFFYCTDESKELERCQYLDYEKEVEAQPROWKKY-- 1329
Qy 161 STDHMYVPPQLGITVVVIALIPGIALFLVLPVCGVHLLRELGLSSISLYSYVTTTIG 220
Db 1330 --DFHYDNVLMALLFTVSTGEG-----WPMVLKH-----SVDATYE----- 1365

Qy 221 PGDYVPTFGANQPKFEGFWVYQIFVIVWFIF-SLGYLVMIIMTIFTRG-----LQS 271
Db 1366 --EQGPSGPGYRM--ELSFYVYVY--FVVPFFVNFVIALIIITFQEGDKVMSCSLEK 1419

Qy 272 KKLAYLEQQLSS-----NLKATQNRIVSGVTKDGYLRRLMLNELYLKVKPVYTDV 322
Db 1420 NERACIDFAISAKPLTRYMPQNRQSFQKWTFFVVSPP-----FEYFIMAMIALNTVV 1472

Qy 323 -----DIAYTLPRNSCPDL---SMYRVEPAPIPSRKRAFVSCADVMVGAQREAGMVHAN 373
Db 1473 LMKFYDAPYEYELMLKCLNIVFTSMFSME-----CVLKITA---FGVLNYF 1516

Qy 374 SDTDLTKLDREKTFGTAEAYHOTDLLAKVVNALATVKPPPAEQDAALYGYHGFSDSQ 433
Db 1517 RDA-----WNFVDFVTVLGSITDILVTEI-----AICPRRFQOCYSTPG----- 1557

Qy 434 ILASEWSFSTVNEFT-----SPRRPRARACS-DFNLEAPRWQSERPLRS----- 476

Db 1558 -----VTVTLTHQORRICPVSHSPRSPLSLESASKEPPLVSPVFGSERVIOQFTGI 1609
QY 477 --SHNEWTSGDNOQIOEA-FNORYKQOQRANGAANSTVHLEPDALAEOLRNHRVPVA 533
Db 1610 TVSRNSWKRTISTSSASSASFELR-----GSSCSARATPSA-----SCCGPLS 1652
QY 534 SRSSPC-RMVCDV-CFPRSRRTPRIWSASC-----PWSRYPRVSSRRKPDPRWTTTST 585
Db 1653 SPSRPCPTCVCSLPCCSS--STP-----SSACRCLGILPWNMTTASTA-----TTTSG 1698
QY 586 RSRPPVPNICATDAVHRPSNRMAAPAA 615
Db 1699 RF-----CKPCCCGAPRGPRGTR-SCCPAA 1723

RESULT 15
US-08-311-363-13
; Sequence 13, Application US/08311363
; Patent No. 5876958
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,363
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-51506
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1754 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-311-363-13

Query Match 3.0%; Score 100; DB 2; Length 1754;
Best Local Similarity 21.2%; Pred. No. 0.69;
Matches 121; Conservative 69; Mismatches 184; Indels 196; Gaps 34;
QY 120 MIMAYSGVIGIPVNGILFAG-----LGEYFG---RTEAIVRYRYKKYKM 160
Db 1276 LWFIFAVIAVQ-----LFKGKFFYDSEKELRCRGQILDYEKEVEAQPQWKY--- 1329
QY 161 STDHMYVPPQLGITTVIALIPGIALFLVPCVGVHLLRELGLSSISLYSYVTITIG 220

Db 1330 --DFHYDNVLMALLTLTFTVSTGEG-----WPMVLKH-----SVDATYE----- 1365
QY 221 FGDYVTFEGANQPKFCGWFVYVQIEVIVWFIF-SLGYLVMTMTFITRG-----LQS 271
Db 1366 --EQGSPSPGYRM--ELSIIFYVY--FWVTPFFVFNIFVALIITITFOEGDKVMSECSLEK 1419
QY 272 KKLAYLEQQLSS-----NLKATQNRIWSGVTKDVGYLRRMLNELYLTKVKPVYTDV 322
Db 1420 NERACIDFAISAKPLTRYMPQNFQYKWTWTFVVSPP-----FEYFIMAMIALNTVV 1472
QY 323 -----DIAYTLPRNSCPDL-----SMRYVEPAPIPSRKRAFSCVADMVGQAQRAGMVHAN 373
Db 1473 LMKFYDAPYEYELMLKCLNIVFTSMFME-----CVLKIIA---FGVLNYF 1516
QY 374 SDTDLTKLDREKTFETAAYHQTDTLLAKVNVNALATVKKPPAEQEDAAALYGGYHGSDSQ 433
Db 1517 RDA-----WNFVDFVTVLGSDITDILVTEI-----AICPRRFQFCYSTPG----- 1557
QY 434 ILASEWSFSTVNEFT-----SPRRPRARACS-DENLEAPRWOSERPLRS----- 476
Db 1558 -----VTVTLTHQORRICPVSHSPRSPLSLESASKEPPLVSPVFGSERVIOQFTGI 1609
QY 477 --SHNEWTSGDNOQIOEA-FNORYKQOQRANGAANSTVHLEPDALAEOLRNHRVPVA 533
Db 1610 TVSRNSWKRTISTSSASSASFELR-----GSSCSARATPSA-----SCCGPLS 1652
QY 534 SRSSPC-RMVCDV-CFPRSRRTPRIWSASC-----PWSRYPRVSSRRKPDPRWTTTST 585
Db 1653 SPSRPCPTCVCSLPCCSS--STP-----SSACRCLGILPWNMTTASTA-----TTTSG 1698
QY 586 RSRPPVPNICATDAVHRPSNRMAAPAA 615
Db 1699 RF-----CKPCCCGAPRGPRGTR-SCCPAA 1723

Search completed: March 17, 2001, 19:58:38
Job time: 2020 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2001, 19:25:53 ; Search time 69.96 Seconds
(without alignments)
599.809 Million cell updates/sec

Title: us-08-816-011c-2
Perfect score: 3283
Sequence: 1 MSPNRWILLIFYSYLMFG.....DAVRHRPSNRMAWPAAG 618

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.66:*
1: Pirl:*
2: pirl:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2652	80.8	1001	2 T13807	potassium channel
2	264.5	8.1	551	2 T16436	hypothetical prote
3	264.5	8.1	555	2 T43357	potassium channel
4	264	8.0	393	2 T25392	hypothetical prote
5	247	7.5	523	2 T23373	hypothetical prote
6	242	7.4	452	2 T21118	hypothetical prote
7	239	7.3	336	2 S65566	inward rectifier p
8	238.5	7.3	364	2 T43361	probable potassium
9	233.5	7.1	329	2 T43509	probable potassium
10	233	7.1	334	2 T19860	hypothetical prote
11	232	7.1	485	2 T24201	hypothetical prote
12	231	7.0	336	2 T32347	outward rectifier
13	229.5	7.0	631	2 T26232	hypothetical prote
14	229	7.0	461	2 T43394	potassium channel
15	227.5	6.9	528	2 T21834	hypothetical prote
16	227.5	6.8	325	2 T15584	hypothetical prote
17	223	6.8	513	2 T28933	hypothetical prote
18	222.5	6.8	586	2 T21683	hypothetical prote
19	220.5	6.7	504	2 T22269	hypothetical prote
20	220.5	6.7	539	2 T23700	hypothetical prote
21	217.5	6.6	643	2 T26616	hypothetical prote
22	216	6.6	1136	2 T26953	hypothetical prote
23	215	6.5	335	2 S44635	f22b7.7 protein -
24	211.5	6.4	484	2 T43529	probable potassium
25	211.5	6.4	519	2 T16629	hypothetical prote
26	210	6.4	522	2 T24265	hypothetical prote
27	204.5	6.2	475	2 T27725	hypothetical prote
28	203	6.2	1539	2 T30037	hypothetical prote
29	201.5	6.1	392	2 T45032	hypothetical prote

30	200.5	6.1	769	2	T27550	hypothetical prote
31	190.5	5.8	444	2	T26229	hypothetical prote
32	190	5.8	524	2	T23907	hypothetical prote
33	189	5.8	383	2	T23746	hypothetical prote
34	188	5.7	443	2	T21598	hypothetical prote
35	184	5.6	700	2	T2736A	hypothetical prote
36	177.5	5.4	290	2	T18706	hypothetical prote
37	172	5.2	576	2	T43363	potassium channel
38	170.5	5.2	544	2	T43364	potassium channel
39	166.5	5.1	381	2	T43393	potassium channel
40	165.5	5.0	347	2	T21067	hypothetical prote
41	165	5.0	350	2	T15178	hypothetical prote
42	163	5.0	427	2	T27681	hypothetical prote
43	160.5	4.9	383	2	T23182	hypothetical prote
44	159.5	4.9	405	2	T21188	hypothetical prote
45	159	4.8	681	2	T19429	hypothetical prote

ALIGNMENTS

RESULT 1
T13807
potassium channel protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C:Accession: T13807
R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
A:Title: ORK1, a potassium-selective leak channel with two pore domains cloned from D
A:Reference number: Z17770; MUID:97075152
A:Accession: T13807
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1001 <GOL>
A:Cross-references: EMBL:U55321; NID:g3808067; PID:g3808068; PIDN:AAC69250.1
C:Genetics:
A:Gene: ORK1
A:Map position: 1

Query Match	80.8%	Score	2652	DB 2:	Length	1001;			
Best Local Similarity	90.9%	Pred. No.	1.3e-205;						
Matches	518;	Conservative	10;	Mismatches	32;	Indels	10;	Gaps	4;
Oy	1	MSPNRWILLIFYSYLMFGAAIYVHIEGEEKISRAEORAKQAIANEYLLLELGDKNNT	60						
Db	1	MSPNRWILLIFYSYLMFGAAIYVHIEGEEKISRAEORAKQAIANEYLLLELGDKNNT	60						
Oy	61	TODEILQRISDYCDKPVTLPPYDDPTWTYFHAFFFAFTVCSYGVGNISPTTFAGRM	120						
Db	61	TODEILQRISDYCDKPVTLPPYDDPTWTYFHAFFFAFTVCSYGVGNISPTTFAGRM	120						
Oy	121	IMAYSIGTIPVNGILFAGLGEYFGRTFAIYRKYKMSMDMHVVPOLGLITTVIA	180						
Db	121	IMAYSIGTIPVNGILFAGLGEYFGRTFAIYRKYKMSMDMHVVPOLGLITTVIA	180						
Oy	181	LIPGIALFLVPCGVHLLRELGLSSISLYSVYVTTTTIGFDYVPTFGANQPKFEGGW	240						
Db	181	LIPGIALFLVPCGVHLLRELGLSSISLYSVYVTTTTIGFDYVPTFGANQPKFEGGW	239						
Oy	241	VYQIFVIVWFIFSLGYLVIMTFITRGLQSKKLAYLEQQLSSNLKATONRIWSGVTKDV	300						
Db	240	VYQIFVIVWFIFSLGYLVIMTFITRGLQSKKLAYLEQQLSSNLKATONRIWSGVTKDV	299						
Oy	301	GYLRMLNELYLKVKPVYTDVDIATLPRNSCPDLSMYRVEPAPISPKRFAFSCADM	360						
Db	300	GYLRMLNELYLKVKPVYTDVDIATLPRNSCPDLSMYRVEPAPISPKRFAFSCADM	359						
Oy	361	VGAQREAGMVHANSDDTLTKLDREKTFETAEAYHOTDILAKVNVNATVKPPPAQEDA	420						
Db	360	VGAQREAGMVHANSDDTLTKLDREKTFETAEAYROTDDLAKVNVNATVKPPPAQEDA	419						

QY 421 ALYGGYHGFSDSQAISEWSEFVNEFTSPRRPRARACSDNFLEAPRWQSERPLRSSHNE 480
Db 420 ALYGGYHGFSDSQAISEWSEFVNEFTSPRRPRARACSDNFLEAPRWQSERPLRSSHNE 479
QY 481 WTSWGDNQIQEAFNORYKQQRANGAANSTMVHLEPDALAEOLRNHRVPPVASRSSPCR 540
Db 480 WTSWGDNQIQEAFNORYKQQRANGAANSTMVHLEPDALAEOLK--QSPGAGRVKKFS 537
QY 541 MVGDV--CFPSRRSTP-----RRWSASCP 563
Db 538 MPDGLRLFPFQKRPSODLERKLSVSVSP 567

RESULT 2
T16426
hypothetical protein F52E4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C:Accession: T16426
R:Martin, J.
submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid F52E4.
A:Reference number: Z16512
A:Accession: T16426
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-551 <MAR>
A:Cross-references: EMBL:U56964; NID:g1293826; PID:g2078439; PIDN:AAB54033.1; GSPDB:GNOC
A:Experimental source: strain Bristol N2; clone F52E4
C:Genetics:
A:Gene: CBSP.F52E4.4
A:Map position: x
A:Introns: 14/3; 65/3; 95/2; 118/1; 165/3; 267/1; 297/2; 334/3; 385/2; 477/1; 513/2

Query Match 8.1%; Score 264.5; DB 2; Length 551;
Best Local Similarity 23.3%; Pred. No. 2.3e-13;
Matches 151; Conservative 78; Mismatches 234; Indels 185; Gaps 33;

QY 9 LLIFYISYLMFGAAIYYHIE---HGEEKISRABQRAQIAINEVYLEEL--GDKNTTOD 63
Db 25 LLMVLVLYSFLGFIQRIETNAHAEMKNERINRTACVS---QILHSIHRWSHNOHKV 81
QY 64 EILQRTSDYCDKPVTLPPYDDPTTYTFFYHAFVFTVSTVGVYGNISPTTFAGRMIMI 123
Db 82 QVAEDIAD-CFEP-----EKDERSEWNVFATLYGFGIVTTLGYNRIAPITVYGRMFCI 134
QY 124 AYSVIGIPVNGILFAGLGEYFG-----RTPEAIYRYKK-----YKMSDMMHY 166
Db 135 VYGICGIPVTMIILANGVQYLNNGFAGDSRRKIEA-YRQORRMKSLACKIYKES----- 189
QY 167 VPPQLGLITTVIALIPGIALFLVPCVGVHLL-----RELGLSSISLYSYVTTTIGFG 222
Db 190 -----IQVTSIAL---LCVFLIYVAVGALLPLNGELDFEN-GLYFNFLCLTAIDFG 238
QY 223 DYVPTGANOPKEFGWVYQIFVIVWFISGLYLVMIWMTFTTRGLQSKKLAYLEQQLS 282
Db 239 QLVF-----IRVELLPITFLYVCIGLAITTIATINIGSEYMKKLHYWGKKMK 284
QY 283 SNLKATONRIWSGVTKDVGYLRLMELYLKVKPVYTDVDTAYTLPRNSCPDLSMYRV 342
Db 285 N---AAQTRIFWGGK-----TLKVR-----DLLHAV--GKKC-----GV 313
QY 343 EPAPISRRKRAFSVCADMVGAOREAGMVHANSDDLTKLDREKTFETABAYHOTDOLLA 402
Db 314 EP-----GMIDA---LDLENV-VERTIAMQEGREPPEDLNDE 346
QY 403 VVNALATVPPPAEQDAALYGGYHGFSDSQAISEWSEFVNEFTSPRRPRARACSDNF 462
Db 347 -----PPREP-----SPRSIIHSPCSTRPSNPMPSPSPREDHPFIK 384
QY 463 LEAPRWQSERPL-----RSSHNEWTSGNQIOE-AFNQRYKGOORAN----- 505

Db 385 MDAPAPRSPPLPAYELDTKKPIFQALSNEFM-----NQSAQEKLFNDLDTFQIEINTELV 440
QY 506 -GAANSTMVHLEPDALAEOLRNHRVPPV-----ASRSSPCRMVCDVCFPSRRS-----TPRR 556
Db 441 EDHKESVIIIEPPATFEDMTIQHSILCVDEYEREKVPKR-----FREKKEMYGRDPRK 494
QY 557 IWSA-SCPWSRYPRVSRRRKPPDRPTTTSTRSRPPVNPICATDAVRH 603
Db 495 LYETQIEWDRLERLSD-RKHGPRKRSVLNLSNCSPEVS-SPSPIRH 540

RESULT 3
T43357
potassium channel chain n2p16 homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T43357
R:Wang, Z.W.; Kunkel, M.T.; Wei, A.; Butler, A.; Salkoff, L.
Ann. N. Y. Acad. Sci. 868, 286-303, 1999
A:Title: Genomic organization of nematode 4TM K+ channels.
A:Reference number: Z22446; MUID:99342707
A:Accession: T43357
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-555 <MAN>
A:Cross-references: EMBL:AF083645; PIDN:AAC32856.1

Query Match 8.1%; Score 264.5; DB 2; Length 555;
Best Local Similarity 23.3%; Pred. No. 2.3e-13;
Matches 151; Conservative 78; Mismatches 234; Indels 185; Gaps 33;

QY 9 LLIFYISYLMFGAAIYYHIE---HGEEKISRABQRAQIAINEVYLEEL--GDKNTTOD 63
Db 29 LLMVLVLYSFLGFIQRIETNAHAEMKNERINRTACVS---QILHSIHRWSHNOHKV 85
QY 64 EILQRTSDYCDKPVTLPPYDDPTTYTFFYHAFVFTVSTVGVYGNISPTTFAGRMIMI 123
Db 86 QVAEDIAD-CFEP-----EKDERSEWNVFATLYGFGIVTTLGYNRIAPITVYGRMFCI 138
QY 124 AYSVIGIPVNGILFAGLGEYFG-----RTPEAIYRYKK-----YKMSDMMHY 166
Db 139 VYGICGIPVTMIILANGVQYLNNGFAGDSRRKIEA-YRQORRMKSLACKIYKES----- 193
QY 167 VPPQLGLITTVIALIPGIALFLVPCVGVHLL-----RELGLSSISLYSYVTTTIGFG 222
Db 194 -----IQVTSIAL---LCVFLIYVAVGALLPLNGELDFEN-GLYFNFLCLTAIDFG 242
QY 223 DYVPTGANOPKEFGWVYQIFVIVWFISGLYLVMIWMTFTTRGLQSKKLAYLEQQLS 282
Db 243 QLVF-----IRVELLPITFLYVCIGLAITTIATINIGSEYMKKLHYWGKKMK 288
QY 283 SNLKATONRIWSGVTKDVGYLRLMELYLKVKPVYTDVDTAYTLPRNSCPDLSMYRV 342
Db 289 N---AAQTRIFWGGK-----TLKVR-----DLLHAV--GKKC-----GV 317
QY 343 EPAPISRRKRAFSVCADMVGAOREAGMVHANSDDLTKLDREKTFETABAYHOTDOLLA 402
Db 318 EP-----GMIDA---LDLENV-VERTIAMQEGREPPEDLNDE 350
QY 403 VVNALATVPPPAEQDAALYGGYHGFSDSQAISEWSEFVNEFTSPRRPRARACSDNF 462
Db 351 -----PPREP-----SPRSIIHSPCSTRPSNPMPSPSPREDHPFIK 388
QY 463 LEAPRWQSERPL-----RSSHNEWTSGNQIOE-AFNQRYKGOORAN----- 505
Db 389 MDAPAPRSPPLPAYELDTKKPIFQALSNEFM-----NQSAQEKLFNDLDTFQIEINTELV 444
QY 506 -GAANSTMVHLEPDALAEOLRNHRVPPV-----ASRSSPCRMVCDVCFPSRRS-----TPRR 556
Db 445 EDHKESVIIIEPPATFEDMTIQHSILCVDEYEREKVPKR-----FREKKEMYGRDPRK 498
QY 557 IWSA-SCPWSRYPRVSRRRKPPDRPTTTSTRSRPPVNPICATDAVRH 603


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Query Match          7.1%; Score 233.5; DB 2; Length 329;
Best Local Similarity 26.8%; Pred. No. 3.6e-11;
Matches 79; Conservative 47; Mismatches 96; Indels 73; Gaps 11;

QY 5 RWILLIFYSILMFGAIIYHIEGEEKISRAEQKQIAINEYLLELGLDKNTTQDE 64
DB 7 RTLSLIIVCTLVLLVGAADFDALENEIL-----ORKLVORVREKLKYKNSN----- 56

QY 65 ILQIRSDYCDKVPPLPTTY-DPTPTWTFYHAFFAFTVCSVGYGNISPTTFAGRMIMI 123
DB 57 -----ADVEILLEATIVKSVPHKAGYQWFGAGFYATTIVTIGYGHSTPMTDAGKVFQM 111

QY 124 AYSVIGIPWNGILFAGLGEYFGRTEFA-----IYRKYKYMSTDMHYVPPOLGLITVV 178
DB 112 LYALAGIPLGLIMFQSIGERM-NTPAAKLLRIRRAAGKQPIVTS----- 157

QY 179 IALIPGIALFLVPCVGVHLLRELG-----LSSI-----SLYYSVVTITIGFDYVPT 227
DB 158 -----LIIFCTGWGLLIFGGAFFSSYENWTYFDVAYYCFVLTITIGFDGYVAL 207

QY 228 FG-----ANQPKFEGWFFVYQIFVIFWFFSLGYL-----VMIMTFITRGLQSK 273
DB 208 QKRSLOQTOPE-----YVFFSLVFLFGLTVISAAANLLVRLFTMTEDER 254

RESULT 10
T19860
hypotheical protein C40C9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19860
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188
A:Accession: T19860
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-334 <WIL>
A:Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.1
A:Map position: X
A:Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match          7.1%; Score 233; DB 2; Length 334;
Best Local Similarity 23.1%; Pred. No. 4.1e-11;
Matches 66; Conservative 62; Mismatches 92; Indels 56; Gaps 10;

QY 5 RWILLIFYSILMFGAIIYHIEGEEKISRAEQKQIAINEYLLELGLDKNTTQDE 64
DB 10 RALLILSTFTVLLFCAMVFDKLE-----SEKDTWVRDE 43

QY 65 ILQIRSD-----YCDKVPVLPPTDYDPTPTWTFYHAFFAFTVCSVGYGNI 111
DB 44 I-ERITDRLKHKYNFSERDLHLFEAIAIKSIPQAGYQWQFAGAFYFATVITVGYGHS 102

QY 112 SPTTFAGRMIMAYSIGVIGIPVNGILFAGLGEYFGRTEFAIYRKYKYMSTDMH----- 165
DB 103 APSTWAGKLFQCMIFALGVPMGLIMFQSIGERY-NFTFA-----YSLHFRDLSHQOGFTC 157

QY 166 ----YVPPOLGLITVV--IALIPGIALFLVPCVGVHLLRELGLSSISLYSVVTTTIG 220
DB 158 LQEVPTTHLLMVSLTIGFMVIVSGTYMF-----HTIEKWSIFD-AYFCMITFTSIG 208

QY 221 FGDYVPTFGANQPKFEGWFFVYQIFVIFWFF--IFSLGLVLMIMTFTI 265
DB 209 FGDVLPLQOVNALQDQPLVVFATIMFILGLAVFSAACVNLVLLVGM 254

RESULT 11
T24201
hypotheical protein R12G8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24201
R:Basham, V.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19853
A:Accession: T24201
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-485 <WIL>
A:Cross-references: EMBL:Z93782; PIDN:CAB07854.1; GSPDB:GN00023; CESP:R12G8.2
A:Experimental source: clone R12G8
C:Genetics:
A:Gene: CESP:R12G8.2
A:Map position: 5
A:Introns: 74/1; 162/3; 210/1; 288/1; 339/3; 426/3

Query Match          7.1%; Score 232; DB 2; Length 485;
Best Local Similarity 24.8%; Pred. No. 8.1e-11;
Matches 97; Conservative 60; Mismatches 140; Indels 94; Gaps 16;

QY 5 RWILLIFYSILMFGAIIYHIEGEEKISRAEQKQIAINEYLLELGLD-----KNT 59
DB 92 RYIALLVLAITYLLGATVYFLIEGSNEK-SRLHVREQNL---DKLLDELATVLSAVND 147

QY 60 TTQDEILQIRSDYCDKVPVLPPTYDD-----TPY-----TWTFYHAFFAFTVCSV 106
DB 148 PQSSEHQMKFFIESYISLQKHEEQYKSTYYRLEHDPDNLKWTFSSAFFSMNVYTTT 207

QY 107 GYGNISPTTFAGRMIMAYSIGVIGIPVNGILFAGLGEYFGRTEFAIY-----RKYK 159
DB 208 GYGSISAQTFSGQLFTMIYAFCFVPTLVILRDGLQGMFLVNETKLYAHGLTAVRRIRGR 267

QY 160 MSTDMHYVPPOLGLITVVIALIPGIALFLVPCVGVHLLREL-----GLSSI-SLY 211
DB 268 EYDEDEIQLPIKFCMTILIA-----YLLCTTFVLYLDVAVMGPEWDDGLPYTAFYF 320

QY 212 SVYVTTTTIGFDYVPTFGANQPKFEGWFFVYQIFVIFWFFSLGYLVIM-----TFIF 266
DB 321 SFISLITGLGDVMPNNVYAPP-----VSMIFFGMVTKVYNRATFIIV 366

QY 267 -----RGLQSKKILAYLEQQLSSNLKATQN-----RIWSGYT---KDVG 301
DB 367 ENGVFGLMTLAETKISMLLTERKPGVKTVRS*SSGSSAESVDSKEPRGDFGSDSGDDG 426

QY 302 YLRRLNELYILKVPVYTDVDTIATVLPKSN 332
DB 427 VINRRNEM-----MNTFTVRSIA-TFMRSN 451

RESULT 12
T32347
outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32347
R:Murray, J.; Wohldmann, P.; O'Neal, D.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid F34D6.
A:Reference number: Z21153
A:Accession: T32347
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-336 <MUR>
A:Cross-references: EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:F34D6.3
A:Experimental source: strain Bristol N2; clone F34D6
C:Genetics:
A:Gene: twk-23; CESP:F34D6.3
A:Map position: 2
A:Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3
```

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000 FIA-----VENGIFGAFTLVENKLDLAIVTRSSA-----SVKP----- 531
QY 324 IAYTLPRNSCPDLMSRYVEPAP-IPSRKRAFSVCADMVGAQREAGMVHANSIDTDLTKLD 382
DB 532 -----EDRSTPKVRALS-----DAG----- 549
QY 383 REKTETAETAEYHQTTDLLAKVVNALATVKPPPAEQEDAALYGGVHG-----FSDS 432
DB 550 -----SEVDQETPN-----EILNLTVRSTATFMKSADIYGGGFRVQLRRGDLIHSDS 599
QY 433 QILASEWSFSTVNEFTSPRRPRA 455
DB 600 Q-----NQMTVMSQSLRHRTA 616

RESULT 14
T43394
potassium channel chain n2p18 homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T43394
R:Kunkel, M.T.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in C. elegans.
A:Reference number: Z22479
A:Accession: T43394
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-461 <KUN>
A:Cross-references: EMBL:AF083650; PIDN:AAC32861.1

Query Match 7.0%; Score 229; DB 2; Length 461;
Best Local Similarity : 22.8%; Pred. No. 1.3e+10;
Matches 112; Conservative 78; Mismatches 164; Indels 138; Gaps 21;

QY 7 ILLIIFYISLMFGAAIYYHHGEKEIKSAEQKAQ---IAINEYLLEELGDKN-----T 59
DB 22 LLPLIILVAVTLTGAMTFWMEGENEREMILEOKEDELRITRVYKINQLQIKRQRRLM 81
QY 60 TTODEI--LQRIISYCDKPYLPPTDDTPYTWTFFHAFFFAFTVCSTVGYNISPTEFA 117
DB 82 TABEEYNRTAKVLTTQETLGIVPADMKDIHTFLGSIFYCTVYTYIGYGNIVPGTW 141
QY 118 GRMIIMAYSIVIGPVNGILFAGIGEYFGRTFEAIYRKYKK--MSTDH----- 165
DB 142 GREATTLYAFIGPLTVLSLYCLGSLFAGCKMLWRFLKSTRVSKDSLKNKISEAADNI 201
QY 166 -----YVP-----PQGLLITTVIALIPGIALFLVPCGVHLRELGL 204
DB 202 EEGTAITPSAEKTENNDDLLSFISGLLIIIVWIFCAVLFT-----FLEWDF 253
QY 205 SSISLASYVYTTTTIGDGYVPYFPGANQPKEFGWFVYQIFVIVWPFISSLGVLVMIMTF 264
DB 254 GT-SLFTLTSFTTIGEGDILPS-----DYDFMPVGVLLLLIG-LSLYSTV 297
QY 265 ITRGLOSKKIAYLEQQULSSNLKATQNRSVGTQDVGYLRMRMLNELYLKVKPYTVDVI 324
DB 298 MT-----LIQQOTEALASGMKDNI-----DOEY-ARALNE----- 326
QY 325 AYTLPRNSCPDLMSRYVEPAPIP-SRKRAF-SVCADMVGAQREAGMVHANSDT---DLT 379
DB 327 -----AREDGVD---EHVDPEEPENNKSFDAVISRMWMSKR-GLYILLPOSQKELA 377
QY 380 KLDREKTFETAETHQTDDLAKVVNALATVKPPPBAEQEDAALYGGVHGFSDSQILASEW 439
DB 378 KOSEKKMGKRSIKIQTDNDLLETIR-----BEILKAEL 411
QY 440 SFSTVNEFTSPR 451
DB 412 N-NEMHKYTA PR 422

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121834

Search completed: March 17, 2001, 19:59:57
Job time: 2044 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Query			ID	Description
			Match	Length	DB		
1	1	215	6.5	335	1	TKW8_CAEEL	P34510 caenorhabdi
2	2	131.5	4.0	2312	1	CCAE_HUMAN	Q15878 homo sapien
3	3	127	3.9	691	1	TKO1_YEAST	P40310 saccharomyc
4	4	122.5	3.7	333	1	Y13B_METJA	Q37604 methanococ
5	5	115	3.5	637	1	YHE7_YEAST	P38724 saccharomyc
6	6	114	3.5	2272	1	CCAE_MOUSE	Q61290 mus musculu
7	7	113.5	3.5	425	1	YOCE_ECOLI	P77031 escherichia
8	8	111.5	3.4	343	1	YD57_METJA	Q58752 methanococ
9	9	111	3.4	2222	1	CCAE_RAT	Q07652 rattus norv
10	10	110.5	3.4	2499	1	CIN5_RAT	P15389 rattus norv
11	11	110.5	3.4	2490	1	PIND_HUMAN	Q12923 homo sapien
12	12	105	3.2	552	1	YHN8_YEAST	P38799 saccharomyc
13	13	104	3.2	504	1	RA52_YEAST	P06778 saccharomyc
14	14	102	3.1	506	1	HITB_HAEIN	P71338 haemophilus
15	15	102	3.1	1851	1	CCAA_DROME	P91645 drosophila
16	16	101.5	3.1	390	1	IRKB_MOUSE	Q61743 mus musculu
17	17	100.5	3.1	390	1	IRKB_HUMAN	Q14654 homo sapien
18	18	100	3.0	1558	1	YR83_YEAST	P36028 saccharomyc
19	19	99.5	3.0	334	1	PIT_RHIME	Q30499 rhizobium m
20	20	99.5	3.0	1207	1	DPOL_ASF7	P42489 african swi
21	21	98.5	3.0	160	1	KCSA_STRU1	Q54397 streptomyce
22	22	98.5	3.0	3432	1	POLG_JAEVJ	P32886 j genome po
23	23	98	3.0	522	1	NUSM_MYTED	Q00232 mytilus edu
24	24	98	3.0	1475	1	TRAZ_CAEEL	P34709 caenorhabdi
25	25	97.5	3.0	390	1	IRKB_RAT	P70673 rattus norv
26	26	97.5	3.0	450	1	YOE3_CAEEL	Q17528 caenorhabdi
27	27	97.5	3.0	676	1	CIQ1_HUMAN	P51787 homo sapien
28	28	97.5	3.0	3432	1	POLG_JAEVJ	P27395 j genome po
29	29	96.5	2.9	570	1	HXT1_YEAST	P32465 saccharomyc
30	30	96.5	2.9	604	1	CIQ1_MOUSE	P97414 mus musculu
31	31	96.5	2.9	1227	1	LAFA_HUMAN	P51826 homo sapien
32	32	95.5	2.9	767	1	HYPF_SYNP3	Q55638 synecocyst
33	33	95.5	2.9	1794	1	YAV1_SCHY3	Q10172 schizosacch

RESULT 1.

```

TWK8. CAEEL. STANDARD; PRT; 335 AA.
ID P34410;
AC AC
AD 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE TWK-8 PROTEIN.
DE TWK-8 OR F22B7.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RC MEDLINE=94150718; PubMed=7906398;
RR Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RR Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RR Craxton L., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RR Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RR Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RR Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RR Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RR Slings M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden K.,
RR Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RR Waterson R., Watson A., Weinstein L., Wilkinson-Sproat J.,
RR Wohldman P.;
RR "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RR elegans."
RR Nature 368:32-38(1994).
RL -1- SIMILARITY: TO POTASSIUM CHANNEL PROTEIN HAK-6.
CC -----
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CC WORMPEP; F22B7.7; CE00160.
CC SEQUENCE 335 AA; 38472 MW; 27DE7F1E79B3CA29 CRC64;
CC -----

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Query Match 6.5%: score 215: DB 1: Length 335:

Best Local Similarity 25.38; Pred. No. 9.5e-09;

Matches	77; Conservative	40; Mismatches	95
---------	------------------	----------------	----

[illegible]

89 TWTFYHAAFFFAFTVCS TVGYGNISPTTFAGRMIMIAYSVIGI

[illegible]

27 TWTFSSIFFAVTVTTIGYGNVPVTNIGRIWCILFSLGLI

149 EAIYRRYKKYK-----MSTDMHYV

$\frac{1}{2}$

87 VWLYGNYLKLKYLILSRHRKERREHVCEHCHSHGMGHDMNIE

FT	DOMAIN	1243	1256	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1257	1274	S4 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1275	1293	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1294	1313	S5 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1314	1400	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1401	1424	S6 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1425	1481	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1482	1500	S1 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1501	1515	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1516	1535	S2 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1536	1543	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1544	1562	S3 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1563	1573	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1574	1592	S4 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1593	1611	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1612	1631	S5 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1632	1700	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1701	1726	S6 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1727	2272	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1728	2272	POLY-GLU.
FT	DOMAIN	1729	722	POLY-ARG.
FT	TRANSMEM	751	754	POLY-ARG.
FT	DOMAIN	770	773	POLY-GLU.
FT	TRANSMEM	1108	1112	POLY-LYS.
FT	DOMAIN	1115	1118	POLY-VAL.
FT	TRANSMEM	1231	1234	POLY-ARG.
FT	DOMAIN	2244	2247	POLY-ARG.
FT	TRANSMEM	375	392	POLY-ARG.
FT	SITE	310	310	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	SITE	658	658	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1375	1375	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1666	1666	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	CA_BIND	427	439	BY SIMILARITY.
FT	MOD_RES	1737	1737	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT	CA_BIND	1755	1766	BY SIMILARITY.
FT	CARBOHYD	255	255	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1569	1569	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1692	1692	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	2272	2272	AA; 257233 MW; 70D9200B9E0C87A1 CRC64;
Query Match		3.5%;	Score 114;	DB 1; Length 2272;
Best Local Similarity		19.5%;	Pred. No. 3;	
Matches 118;	Conservative	86;	Mismatches	242; Indels 160; Gaps 25;
QY	90 WTFYHAF	-----FFAFTVGVSTVGYGNI	-----SPTTFAGRMIMIA	124
Db	1601 WTEVQSKALPYVCLLIAMLEFFIYAIIGMQVFGNKLDEESHINRHNFRSFFGSLMLLF	1660		
QY	125 YSVIGIPVNGILFAGLGEYFGRTE	-----AIYRKYKYNSTDMHYVPPQLGTLTTVIA	180	
Db	1661 RSATGEAQWELMSCLGE	-----KCEPDTTAPSGONESERCGTDLAVV	-----YFVSFFFC	1713
QY	181 LIPGIALFLVL	-----PCGVHLLREL	-----GLSSISLYSYVT	215
Db	1714 SFLMLNLFVAVIMDNFEYLRDSSILGPHLDEFVRVWAEYDRAACGRHYTEYEMTL	1773		
QY	216 -TTTIGEGDVPTFGANQPKFEGFVYVIFVI	-----VWFIFSLGLVIMMTFIFRGLQ	270	
Db	1774 MSPPLGLGKRCPS	-----KVAYKRLVLMNPFVAEDMTVHTSTLMALIRALD	1821	
QY	271 SK--KLAYLEQQLSSNLKATONRTWSVTKDGYLRMLNELYLKVKPYTVDVI	-----	324	
Db	1822 IKIAGGADQQLDSELSQKETLAIHPLHSQKMLDILLVPMFKASDLTVGKIYAAMMIDY	1881		
QY	325 -----AYTLPRNSCPDLSMYRVEPAPIPSKRAFSVCADWVGQAQREAGMVHANS	SDT 376		
Db	1882 KQSKVKQROQLLEQKNAP	-----MFQMEPSSLPOEITANAKALPYLQDPVSGLSGRSGYP	1939	

QY	377	DLTKLDREKTFETAEAYHQTTDLLAKVYNVALATVKVPPAQEDAAALYGGYHGFSOIL	435
Db	1940	SMSPLSQEIQF-----LACMDPADGQ-----FQEQQSLV	1970
QY	436	-----ASEWFSFVNEFTSPRRPARACSFENLEAP-----RWQSERPLRSSHNEWTSG	485
Db	1971	VTDPSSMRRSFSTIRD-----KRSNSSLWLEFMSERSSENTYKSR--RSYHSSLRLSAHR	2024
QY	486	-DNOIQEAFNQRYKGOORANGAANSTMVHLEPDALAEQLRNHRVPAVSRSSPCRMVCD	544
Db	2025	LNSDSGHKSTHRSGGRER--GRSKERKHLSPDV--SRCNSEBGTQADWESPERQSR	2080
QY	545	VCPPSRSTPRRIWASCPWSPRYVSSRRKPDPTWTTSTRSR--PPVNP-----ICA	597
Db	2081	SPSEGRSOTNRQGTGSLSESSIPSISD-----TSTPRSRRLQPPVPPRPLLSY	2132
QY	598	TDAVRH 603	
Db	2133	SSLMRH 2138	
RESULT	7		
YQCE_ECOLI			
ID	YQCE_ECOLI	STANDARD;	PRT; 425 AA.
AC	P77031; P76634; P76635;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DE	HYPOTHETICAL 46.8 KDA PROTEIN IN CYSJ-ENO INTERGENIC REGION.		
GN	YQCE.		
OS	Escherichia coli.		
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
OC	Escherichia.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=K12 / MGI655;		
RX	MEDLINE=97426617; Pubmed=9278503;		
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,		
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,		
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,		
RA	Mau B., Shao Y.		
RT	"The complete genome sequence of Escherichia coli K-12."		
RL	Science 277:1453-1474(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=K12;		
RA	Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,		
RA	Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K.,		
RA	Kasai H., Kashimoto K., Kim S., Kimura S., Kitagawa M.,		
RA	Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H.,		
RA	Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,		
RA	Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C.,		
RA	Yamamoto Y., Yano M.		
RL	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).		
-CC	-1- SIMILARITY: TO E.COLI YIHN.		
CC			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC			
DR	EMBL; AE000361; AAC75817.1; --		
DR	EMBL; D90893; CAB22504.1; --		
DR	ECOGENE; EG13174; YQCE.		
KW	Hypothetical protein; Transmembrane.		
FT	TRANSMEM	9	29
FT	TRANSMEM	49	69
FT	TRANSMEM	76	96
FT	TRANSMEM	97	117

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FT TRANSMEM 139 159 POTENTIAL.
FT TRANSMEM 172 192 POTENTIAL.
FT TRANSMEM 220 240 POTENTIAL.
FT TRANSMEM 260 280 POTENTIAL.
FT TRANSMEM 292 312 POTENTIAL.
FT TRANSMEM 314 334 POTENTIAL.
FT TRANSMEM 355 375 POTENTIAL.
FT TRANSMEM 389 409 POTENTIAL.
SQ SEQUENCE 425 AA; 46830 MW; 538C547C7FC52DEA CRC64;

Query Match 3.5%; Score 113.5; DB 1; Length 425;
Best Local Similarity 20.6%; Pred. No. 0.39;
Matches 59; Conservative 42; Mismatches 105; Indels 81; Gaps 12;

QY 8 LLLIYISYLMFGAIIYHIEGEEKISRAEQKQAIANEYLLLELGDKNKTTTODEILO 67
Db 173 VIIIVSVVILGILCWFFVSNNLRSANNEKQSFQSDIL-----AVL 218
QY 68 RISDYCDKVPILPPYDDPPYTFHAFFAFTVCSTVGYGNISPTTFAGRMIMIAYSV 127
Db 219 RIIST-----TWYCSMVIFGVFTIYAILISYNTLYLTEMYG-MSLVAAASY 260
QY 128 IGPVNGILFAGLGEYFRTFEAIYRYKRYKMSYDMHYVPPQLGLITTVV----- 178
Db 261 MGIVINKIFRALCGPLGG-----LITYSKVKSPTFVIOILSVLGLLTLTALLVTSNPDQ 315
QY 179 -TALIPGIALFVLPCVGHLLRELGLSSISLY-----SYVTITIGFGDYVPFT 228
Db 316 SVAMGIGLILLGLFTC-----YASRGLYWACPGEARPTSYIMGTTCVIGSVIGFL 365
QY 229 GANQKEF-----GGW-----FVYQIVFIVWF--IFSLGYLVLMIMPTI 265
Db 366 ----PDVFYPIIGHWQDTLPAAEAYRNMLGMAALG-MVIVFTPL 407

RESULT 8
YD57_METJA STANDARD; PRT; 343 AA.
AC Q58752;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE PUTATIVE POTASSIUM CHANNEL PROTEIN MJ1357.
GN MJ1357.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE-96337999; PubMed-8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinscock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: STRONG, TO M.JANNASCHII MJ0138.1.
CC -!- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNELS.
CC -----
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CC -----
DR EMBL; U67575; AAB99365.1; -.
DR TIGR; MJ1357; -.
KW Hypothetical protein; Transmembrane; Transport; Ion transport;
KW Ionic channel.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 62 82 POTENTIAL.
SQ SEQUENCE 343 AA; 38883 MW; 61231B0C001B54C4 CRC64;

Query Match 3.4%; Score 111.5; DB 1; Length 343;
Best Local Similarity 28.9%; Pred. No. 0.42;
Matches 26; Conservative 21; Mismatches 40; Indels 3; Gaps 2;

QY 92 FYHAFFFAFTVCGTGYGNISPTTFAGRMIMIAYSVIGIPVNGILFAGLGEYF--GRTFE 149
Db 133 YFTALYFSVITITTCYGDFTPKTFLGRVLTVVYLCVGVIVMYLFLSLAEFIVECKFEE 92
QY 150 AIYRYKRYKMYST-DMHYVPPQLGLITTVV 178
Db 93 FVRLKMKMKIKTKDKHYICGYGRGLGVV 122

RESULT 9
CCAE_RAT STANDARD; PRT; 2222 AA.
AC Q07652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-DEPENDENT R-TYPE CALCIUM CHANNEL ALPHA-1E SUBUNIT (CALCIUM
DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE, ISOFORM 6) (RBE-II) (RBE2)
DE (BRAIN CALCIUM CHANNEL II) (BII).
DE CACNALE OR CACNLIA6 OR CAC46.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE-93262464; PubMed-8388125;
RA Soong T.W., Stea A., Hodson C.D., Dubel S.J., Vincent S.R.,
RA Snutch T.P.;
RT "Structure and functional expression of a member of the low voltage-
RT activated calcium channel family."
RL Science 260:1133-1136(1993).
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E
CC GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS
CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
CC BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA).
CC THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-
CC CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-
CC AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE
CC INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS
CC IMPORTANT FOR INFORMATION PROCESSING.
CC -!- SUBUNIT--VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN CENTRAL NERVOUS SYSTEM AND IN
CC INSULINOMA.
CC -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
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POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION. -I- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.

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EMBL; LJ15453; AAA40855.1; -
INTERPRO: IPR000636; -
INTERPRO: IPR002077; -
PFAM; PF00520; Ion_trans; 4.
PRINTS; PR00167; CACHANNEL.
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
Calcium channel; Glycoprotein; Repeat; Multigene family;
Calcium-binding; Phosphorylation.
FT REPEAT 27 305 I.
FT REPEAT 413 657 II.
FT REPEAT 1092 1378 III.
FT REPEAT 1415 1678 IV.
FT DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 41 59 S1 OF REPEAT I (POTENTIAL).
FT DOMAIN 60 78 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 79 97 S2 OF REPEAT I (POTENTIAL).
FT DOMAIN 98 109 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 110 124 S3 OF REPEAT I (POTENTIAL).
FT DOMAIN 125 136 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 137 156 S4 OF REPEAT I (POTENTIAL).
FT DOMAIN 157 174 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 175 195 S5 OF REPEAT I (POTENTIAL).
FT DOMAIN 196 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 S6 OF REPEAT I (POTENTIAL).
FT DOMAIN 302 427 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 428 447 S1 OF REPEAT II (POTENTIAL).
FT DOMAIN 448 460 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 461 480 S2 OF REPEAT II (POTENTIAL).
FT DOMAIN 481 489 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 490 508 S3 OF REPEAT II (POTENTIAL).
FT DOMAIN 509 518 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 519 537 S4 OF REPEAT II (POTENTIAL).
FT DOMAIN 538 556 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 557 576 S5 OF REPEAT II (POTENTIAL).
FT DOMAIN 577 629 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 630 654 S6 OF REPEAT II (POTENTIAL).
FT DOMAIN 655 1100 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1101 1117 S1 OF REPEAT III (POTENTIAL).
FT DOMAIN 1118 1141 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1142 1161 S2 OF REPEAT III (POTENTIAL).
FT DOMAIN 1162 1199 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1170 1192 S3 OF REPEAT III (POTENTIAL).
FT DOMAIN 1193 1206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1207 1224 S4 OF REPEAT III (POTENTIAL).
FT DOMAIN 1225 1243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1244 1263 S5 OF REPEAT III (POTENTIAL).
FT DOMAIN 1264 1350 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1351 1374 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1375 1431 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1432 1450 S1 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1451 1467 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1468 1485 S2 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1486 1493 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1494 1512 S3 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1513 1523 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1524 1542 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1543 1561 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1562 1581 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1582 1650 EXTRACELLULAR (POTENTIAL).

Db 2082. SSMRH 2087

RESULT 10

CIN5_RAT STANDARD; PRT: 2019 AA.

AC P1389; S3 OF REPEAT III (POTENTIAL).

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE SODIUM CHANNEL PROTEIN, CARDIAC MUSCLE ALPHA-SUBUNIT.

DN SCN5A.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

[[1]]

RC SEQUENCE FROM N.A.

RC TISSUE=HEART;

RX MEDLINE=90046760; PubMed=2554302;

RA Rogard R.B., Cribbs L.L., Muglia L.K., Kephart D.D., Kaiser M.W.;

RT "Molecular cloning of a putative tetrodotoxin-resistant rat heart Na+ channel isoform."

RL proc. Natl. Acad. Sci. U.S.A. 86:8170-8174(1989).

CC -!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT. IT IS A TETRODOTOXIN-RESISTANT NA+ CHANNEL ISOFORM.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -!- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -!- MISCELLANEOUS: NA+ CHANNELS IN MAMMALIAN CARDIAC MEMBRANE HAVE FUNCTIONAL PROPERTIES QUITE DISTINCT FROM NA+ CHANNELS IN NERVE AND SKELETAL MUSCLE.

CC -!- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.

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CC -----

DR EMBL; M27902; AAA42114.1;

DR PIR; A33996; A33996.

DR INTERPRO; IPR000048;

DR INTERPRO; IPR000636;

DR INTERPRO; IPR001696;

DR PFAM; PF00612; IQ; 1.

DR PFAM; PF00520; Ion_trans; 4.

DR PRINTS; PR00170; NACHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Duplication; Multigene family; Phosphorylation.

KW TRANSMEM 128 151 S1 OF REPEAT I (POTENTIAL).

FT TRANSMEM 160 179 S2 OF REPEAT I (POTENTIAL).

FT TRANSMEM 193 211 S3 OF REPEAT I (POTENTIAL).

FT TRANSMEM 218 237 S4 OF REPEAT I (POTENTIAL).

FT TRANSMEM 254 277 S5 OF REPEAT I (POTENTIAL).

FT TRANSMEM 391 416 S6 OF REPEAT I (POTENTIAL).

FT TRANSMEM 713 737 S1 OF REPEAT II (POTENTIAL).

FT TRANSMEM 749 772 S2 OF REPEAT II (POTENTIAL).

FT TRANSMEM 781 800 S3 OF REPEAT II (POTENTIAL).

FT TRANSMEM 807 826 S4 OF REPEAT II (POTENTIAL).

FT TRANSMEM 843 863 S5 OF REPEAT II (POTENTIAL).

FT TRANSMEM 917 942 S6 OF REPEAT II (POTENTIAL).

FT TRANSMEM 1203 1226 S1 OF REPEAT III (POTENTIAL).

FT TRANSMEM 1240 1265 S2 OF REPEAT III (POTENTIAL).

Query Match 3.4%; Score 110.5; DB 1; Length 2019;

Best Local Similarity 20.3%; Pred. No. 4.7;

Matches 87; Conservative 68; Mismatches 150; Indels 123; Gaps 21;

Qy 176 TVVIALFGIALFLVLPQGV-----HLLRELGL-----SSISLYSVVVTITG 220

Db 844 TLVLAI--VFIFAV--VGMOLFKNYSELKRLISDSGLLPRWHMDDFFHAFILFRIL 898

Qy 221 FGDIYPTFGANPKFEGWVFVYQIFVWFISGLYLVIMTFTTRGLQSKKLAYL--- 277

Db 899 CGEWTMW--DCMEVSGOSLCLLVFLVWVI---GNLVVNLFLALLSSFSADNLTAP 953

Qy 278 -EQQLSSNLIKATONRWGV-----TKD--VGYLRLMNLNLYILKVPVYTDVDIAYTL 328

Db 954 DEDGEMNNLQALARIQRLREVKRTTWFCCGILRRRPKKAAL---ATHSQLPSCITA 1010

Qy 329 PRNSCPDLSMYRVSPAPIPSEKR-----AFSVCADMVGAQREAGMVHA 372

Db 1011 PRSPPPE-----VEKVP-PARKETFEEDKRPQGTGDPGSEPCVPIAVAE----- 1056

Qy 373 NSDSDLTKLDREKTFETAEAYHQTTDLAKVYNALATVKPPAEQEDALYGYHGFSDS 432

Db 1057 -SDTEQDEDEENSLGTEE-----ESSKOESQVSVSGHEPYQEP 1094

Qy 433 QILASEWFSFTVNEFTSPRRPARACSFNLEAPWQSERPLRSSHNEWTWGSDDNOQIOE 492

Db 1095 R-----AMSQVSETTSSEAGASTSQAD-----WQEQ-----KTEPAQPGCGETPED 1136

Qy 493 AFNORYKGOORANGAANSTWVHLEPDALDEE--QLRNHRVPVVASRSSPCRMVCDVCFPSR 550

Db 1137 SYSE-----GSTADMTNT---ADLLEQIPDLGEDVKDPEDCTEGCVRRCPCMWDT 1185

Qy 551 RSTPRRIW 558

Db 1186 TQSPGKVV 1193

RESULT 11

PTND_HUMAN STANDARD; PRT: 2490 AA.

ID PTND_HUMAN Q15263; Q16826; Q15264; Q15265;

AC Q12923; Q15263; Q16826; Q15264; Q15265;

DT 01-OCT-2000 (Rel. 40, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

RN SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
VIII.";
RL Science 265:2077-2082(1994).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC
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CC
CC EMBL: U10556; AAB68887.1; -
DR PIR: S46809; S46809.
DR SGD: S0001120; YHR078W.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 127 147 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
FT TRANSMEM 393 413 POTENTIAL.
FT TRANSMEM 517 537 POTENTIAL.
SQ SEQUENCE 552 AA; 63330 MW; 8FE0A888937281F CRC64;

Query Match 3.2%; Score 105; DB 1; Length 552;
Best Local Similarity 21.6%; Pred. No. 2.3;
Matches 68; Conservative 50; Mismatches 107; Indels 90; Gaps 14;
QY 31 EKKISRAEQRKAQ-TAINFYLLLEELGDKNTTQDEILQRISSYCDKPVLPPTDYDDTPT 89
DB 256 EEKIQDYEHNEIQVILSRLEEVEE-NSTFKAELEKIAWQLEGLKLEALLQSPQV 314
QY 90 WTFYHAF---FFAFTVCTVGNGNISPTTFAGRMIMAIYSGIPVN----- 133
DB 315 RTFKAFGEFTIYCLHKLI-----ITFLKRIPIYIYHSLKYPDDYDNFSENAASD 367
QY 134 --GILFAGGEVGRFTFEAIYRRYKMYKMTDMHYVPPOLGLI-----TTV 177
DB 368 PLATYIANILDF-----SFFRFNYQHDLSLTKQISLSLSLFLCCLSAVNTTI 417
QY 178 --VIALIP---GIALFL-----VLP-----CVGVHLLRELGLS 205
DB 418 SYVVTLLPKFQILALFAMQNDTANVLPETYNNSYKGGKKNYSOEQKGISLKNLVVS 477
QY 206 SISLSYSYVTTTIGDGVPTFEGANQPKF-EGGFVYVQIIVVWF-----IFSLGYLVW 260
DB 478 EIT--GVVYLATLTVRSHLPFVSQRLKELGKFTVFNIVDSWFDVYAFACVFTFI 535
QY 261 IMFTITRGLQSKLA 275
DB 536 CIRIAERKLSTKKVS 550

RESULT 13
RA52.YEAST
ID RA52.YEAST STANDARD; PRT: 504 AA.
AC P06778;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE DNA REPAIR AND RECOMBINATION PROTEIN RAD52.
GN RAD52 OR YML032C.

OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85137465; PubMed=6098821;
RA Aduma K., Ogawa T., Ogawa H.;
RT "Primary structure of the RAD52 gene in Saccharomyces cerevisiae.";
RL Mol. Cell. Biol. 4:2735-2744(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Badcock K., Churcher C., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN DOUBLE-STRAND BREAK (DSB) REPAIR AND
CC RECOMBINATION.
CC -!- SUBUNIT: PART OF A COMPLEX THAT INCLUDES RAD51 AND RAD52.
CC -!- SIMILARITY: BELONGS TO THE RAD52/RAD22 FAMILY.
CC
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CC
CC EMBL: M10249; AAA50352.1; -
DR EMBL: Z46659; AAA86623.1; -
DR PIR: A23282; A23282.
DR SGD: S0004494; RAD52.
KW DNA recombination; DNA repair.
SQ SEQUENCE 504 AA; 56063 MW; 590C3700B1B8058 CRC64;

Query Match 3.2%; Score 104; DB 1; Length 504;
Best Local Similarity 18.7%; Pred. No. 2.4;
Matches 96; Conservative 71; Mismatches 181; Indels 166; Gaps 24;
QY 192 PCGVGH-----LRELGLSISLSYSYVTTTITGFGD-----YVPTFG---ANPKPF 236
DB 45 PVFGNHSEDIQTKLKKLGPYIS-----KRVGFTSRATIEGWRVINLANQIFY 96
QY 237 GGFVVYQIVVWFI-----FSLGYLVIMTFTTRGLQSKLAYLEOOLSNLKATON 290
DB 97 NGWSTEVK-SVVIDFLDERQGFSGICTAIVRVTLTSGTYREDIGYGTVENERRKPAAFE 155
QY 291 RIWSGVTKDV-----GYLRRLNELY-----ILKVK-----PVYTDVDIAYTL 328
DB 156 RAKKSAVTDAKRSURGFNGALNCLYDKFLAKIDKVKFDPDPDENLFRPTDISES 215
QY 329 PRSNPCDLSMYRVEPAPISRRKRAFSCAD-----MVGQAREA 367
DB 216 SRTNLTIE---NQEQOQYFNKRRLTKVTNTNPDSKTNLVKIENTVSRGTPMAAPAEA 271
QY 368 GMVH-ANSTDTLTKLDREKTFETAEAYHQTDLAKVVALATVPKPPAEQEDAAALGYG 426
DB 272 NSKNSNKKDITLKLSDASK-----QQQDILL-----DDSLMFS-- 304
QY 427 HGFSDSOILASEWSPSTVNEFTSPRP-----RARACSDFNLEAPWQSERPLRSSHNEW 481
DB 305 DDFQDDLLI--NMGNTNSNVLTEKDPVVAQKOSPTASSNPEAEITFTVAKAATSVQNE- 361
QY 482 TWSGDNOQIQEAFNORYKGQQRANGAANSTMVHLEPDALDEO----- 523
DB 362 RYIGE-----ESIFDPKYQAQSRHTVDTQTSKHIPASVLKDKTWTARTDSVYEKFAPKG 417
QY 524 ----LRNN-----HRVPVARSPPCMVCDVCFPPSRRTPRRIWSASCPSWRYPRVSSRR 574
DB 418 QLSMKNNDKELGPHMLEGAGNQVP-----RETTPIKTNATAFPPAAAPRAPPSS 466
QY 575 K---PD-----PRWTTTSTRSRPPVNPICA 597

Db 467 KWHPNGNGAVPAVPOQRSTRREVGRKINPLHA 500

RESULT 14

```
HTB_HAEN STANDARD; PRT; 506 AA.
AC P71338; Q53440;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE IRON(III)-TRANSPORT SYSTEM PERMEASE PROTEIN HTB.
GN HTB OR HI0098.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-L., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NTHI TN106;
RX MEDLINE=95012644; PubMed=7927717;
RA Sanders J.D., Cope L.D., Hansen E.J.;
RT "Identification of a locus involved in the utilization of iron by
RT Haemophilus influenzae.";
RL Infect. Immun. 62:4515-4525(1994).
CC -1- FUNCTION: INVOLVED IN A PERIPLASMIC BINDING-PROTEIN-DEPENDENT
CC IRON(III) TRANSPORT SYSTEM.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTW
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; U32695; AAC21774.1; ALT_INIT.
DR EMBL; S72674; AAB32111.1;
DR TIGR; HI0098;
DR INTERPRO; IPR000515;
DR PRAM; PF00528; BPD_transp. 2.
DR PROSITE; PS00402; BPD_TRANS_INN_MEMBR; FALSE_NEG.
DR KW Transport; Iron transport; Transmembrane; Inner membrane.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 57 77 POTENTIAL.
FT TRANSMEM 90 110 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 174 194 POTENTIAL.
FT TRANSMEM 218 238 POTENTIAL.
FT TRANSMEM 275 295 POTENTIAL.
FT TRANSMEM 314 334 POTENTIAL.
FT TRANSMEM 350 370 POTENTIAL.
FT TRANSMEM 379 399 POTENTIAL.
FT TRANSMEM 428 448 POTENTIAL.
```

```
FT TRANSMEM 480 500 POTENTIAL.
FT VARIANT 72 72 F -> L (IN STRAIN TN106).
FT VARIANT 104 104 G -> C (IN STRAIN TN106).
FT VARIANT 116 116 V -> G (IN STRAIN TN106).
FT VARIANT 167 167 S -> F (IN STRAIN TN106).
FT VARIANT 252 252 T -> M (IN STRAIN TN106).
SQ SEQUENCE 506 AA; 56546 MW; ADA28861C1481A1D CRC64;
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Query Match 3.1%; Score 102; DB 1; Length 506;
Best Local Similarity 22.3%; Pred. No. 3.4;
Matches 66; Conservative 46; Mismatches 112; Indels 72; Gaps 13;

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QY 3 PNRMILLIFVISYLMFGAALYYHIEGEEKISRAEO-----RKAQIAINEYLLE----- 52
DB 5 PPFWLTLLIILIGLPCLPFLYILRATEVGLKRSVLLFRPRMAELSLMMLMVCVTI 64
QY 53 ---ELGDKNTTODEILQRI-----SDYCDKPVTLP---PTYDDTPYTWTFYHAFFAFTV 102
DB 65 GAISLG---TFCAFLLEYRFFGKAFFEVAMTLPICIPAF-VSGFTW-----ISLTF 112
QY 103 CSIVGYGNISPTTFAGRMIMAIYVIGIPVNGILFAGLGEYFGRTFAIYRRYKYYKMS 162
DB 113 RVEVFWGTI-----GIMTSSFPPLAYLPVSAIL-----KRLDRSLEEVSLGKSPV 161
QY 163 DMHVVPOLGLITTVVIALIPGIALFLVPCVGVHLLRELGLSSISLYSYVVTITIGFG 222
DB 162 FWAISPOLK-----PATGSSILL--IALHMLVEFGAVSI---LWQFTTFAIFQ 206
QY 223 DYVPTFGANQKPEFGWVYVIFVWFIISLG-----YLVMIINTF 264
DB 207 EYEMSFNNSTAALLSAVLMAICILIVFEGEIFFRGKQTLVHSGKGVTRPYLVKLTSLF 262
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RESULT 15

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CCAA_DROME STANDARD; PRT; 1851 AA.
AC P91645; O01713; O01714;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL TYPE A ALPHA-1 SUBUNIT (CACOPHONY
DE PROTEIN) (NIGHTBLIND A PROTEIN) (NO-ON-TRANSIENT B PROTEIN) (DMCA1A).
GN NBA OR CAC OR NONB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RX SEQUENCE FROM N.A., AND RNA-EDITING.
RX MEDLINE=97141514; PubMed=8987815;
RA Smith L.A., Wang X.J., Peixoto A.A., Neumann E.K., Hall L.M.,
RA Hall J.C.;
RT "A Drosophila calcium channel alpha subunit gene maps to a genetic
RT locus associated with behavioral and visual defects.";
RL J. Neurosci. 16:7868-7879(1996).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=97247730; PubMed=9093853;
RA Peixoto A.A., Smith L.A., Hall J.C.;
RT "Genomic organization and evolution of alternative exons in a
RT Drosophila calcium channel gene.";
RL Genetics 145:1003-1013(1997).
RN [3]
RP VARIANT CAC-S.
RX MEDLINE=98315104; PubMed=9649530;
RA Smith L.A., Peixoto A.A., Kramer E.M., Vilella A., Hall J.C.;
RT "Courtship and visual defects of cacophony mutants reveal functional
RT complexity of a calcium-channel alpha subunit in Drosophila.";
RL Genetics 149:1407-1426(1998).
CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
```


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OM protein - protein search, using sw model

Run on: March 17, 2001, 19:56:18 ; Search time 71.86 Seconds
(without alignments)
1007.995 Million cell updates/sec

Title: US-08-816-011c-2
Perfect score: 3283
Sequence: 1 MSPNRWILLIIFYSYLMFG.....DAVHRHPSNRMAAWPAAAAAG 618

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				%		Description	
Result No.	Score	Match	Length	DB	ID		
1	2652	80.8	1001	5	Q94526	Q94526 drosophila	
2	308.5	9.4	502	11	Q9JK62	Q9jk62 mus musculus	
3	301.5	9.2	398	11	O88454	O88454 mus musculus	
4	301	9.2	499	4	O95279	O95279 homo sapien	
5	299.5	9.1	411	11	P97438	P97438 mus musculus	
6	295.5	9.0	426	4	O95069	O95069 homo sapien	
7	295.5	9.0	538	11	Q9J1S4	Q9j1s4 rattus norv	
8	292.5	8.9	411	4	Q9NYT2	Q9nyt2 homo sapien	
9	286	8.7	419	4	Q9NYG8	Q9nyg8 homo sapien	
10	264.5	8.1	551	5	O20673	O20673 caenorhabdi	
11	264.5	8.1	555	5	O76789	O76789 caenorhabdi	
12	264	8.0	393	5	Q9XU07	Q9xu07 caenorhabdi	
13	251.5	7.7	336	11	Q9Z2T2	Q9z2t2 rattus norv	
14	247	7.5	523	5	O17935	O17935 caenorhabdi	
15	245.5	7.5	336	11	O08581	O08581 mus musculus	
16	242	7.4	374	4	O9NPC2	O9npc2 homo sapien	
17	242	7.4	452	5	O93531	O93531 caenorhabdi	
18	241.5	7.4	340	5	Q9VHE0	Q9vhe0 drosophila	
19	239	7.3	299	11	Q9QX34	Q9qx34 mus musculus	

20	239	7.3	336	4	O00180	O00180 homo sapien
21	239	7.3	409	11	O35111	O35111 mus musculus
22	239	7.3	411	11	O54912	O54912 rattus norv
23	238.5	7.3	364	5	O76790	O76790 caenorhabdi
24	237	7.2	365	11	O9JL58	O9j158 cavia porce
25	237	7.2	395	11	Q9JLD4	Q9jld4 rattus norv
26	235	7.2	398	5	Q9VFS9	Q9vfs9 drosophila
27	233.5	7.1	329	5	O76795	O76795 caenorhabdi
28	232	7.1	485	5	O9XTV6	O9xtv6 caenorhabdi
29	231.5	7.1	394	4	O14649	O14649 homo sapien
30	231	7.0	336	5	O17185	O17185 caenorhabdi
31	229.5	7.0	631	5	O45894	O45894 caenorhabdi
32	229	7.0	461	5	Q9TZP8	Q9tzip8 caenorhabdi
33	229	7.0	654	5	P90863	P90863 caenorhabdi
34	227.5	6.9	259	6	O02821	O02821 oryctolagus
35	226	6.9	307	5	O94253	O94253 caenorhabdi
36	223.5	6.8	325	5	O18120	O18120 caenorhabdi
37	223	6.8	513	5	Q22940	Q22940 caenorhabdi
38	222.5	6.8	586	5	O62209	O62209 caenorhabdi
39	220.5	6.7	504	5	Q93732	Q93732 caenorhabdi
40	220.5	6.7	539	5	Q21505	Q21505 caenorhabdi
41	217.5	6.6	643	5	O9XXF6	O9xxf6 caenorhabdi
42	216	6.6	1136	5	O9XX01	O9xx01 caenorhabdi
43	212	6.5	995	5	Q9W2L7	Q9w2l7 drosophila
44	211.5	6.4	484	5	Q9TZP7	Q9tzip7 caenorhabdi
45	211.5	6.4	519	5	Q21467	Q21467 caenorhabdi

ALIGNMENTS

RESULT 1

Q94526

ID O94526 PRELIMINARY; PRT; 1001 AA.

AC Q94526;

DT 01-FEB-1997 (TREMBlrel. 02, Created)

DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)

DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE OPEN RECTIFIER POTASSIUM CHANNEL PROTEIN 1 (ORK1 PROTEIN) (TWO P

DE DOMAIN POTASSIUM CHANNEL ORK1).

CM ORK1.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Nephelidae; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Beres P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LARVA;
 RX MEDLINE=97075152; PubMed=8917578;
 RA Goldstein S.A.N., Price L.A., Rosenthal D.N., Pausch M.H.;
 RT "Ork1, a potassium-selective leak channel with two pore domains cloned
 RT from *Drosophila melanogaster* by expression in *Saccharomyces*
 RT *cerevisiae*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:13256-13261(1996).
 CC -1- FUNCTION: BACKGROUND POTASSIUM CHANNEL. RECTIFICATION IS DEPENDENT
 CC ON EXTERNAL POTASSIUM CONCENTRATION. ACTS AS AN OUTWARDLY
 CC RECTIFYING CHANNEL BUT AS EXTERNAL POTASSIUM LEVELS INCREASE, THIS
 CC IS REVERSED.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT, STRONGEST
 CC EXPRESSION IN MUSCLE, BRAIN AND OVARY. ALSO PRESENT AT LOW LEVELS
 CC IN LARVA AND EMBRYO.
 CC -1- MISCELLANEOUS: INHIBITED BY BARIUM.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
 CC EMBL: AE003484; AAF47972.1; -;
 DR EMBL: U55321; AAC8250.1; -;
 DR FLYBASE: FBgn0017361; Ork1.
 DR INTERPRO: IPR000099; -;
 DR INTERPRO: IPR001622; -;
 DR PFAM: PF02034; TWIK channel; 1.
 DR PRINTS: PR01333; 2POREKCHANEL.
 KW Ionic channel; Transmembrane; Ion transport; Glycoprotein;
 KW potassium transport.
 FT DOMAIN 1 6 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 7 27 POTENTIAL.
 FT DOMAIN 95 111 PORE-FORMING (POTENTIAL).
 FT TRANSMEM 120 140 POTENTIAL.
 FT DOMAIN 141 170 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 171 191 POTENTIAL.
 FT DOMAIN 208 224 PORE-FORMING (POTENTIAL).
 FT TRANSMEM 244 264 POTENTIAL.
 FT DOMAIN 265 1001 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 58 58 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 1001 AA: 109289 MW; 09AE1A3669072E07 CRC64;

Query Match 80.8%; Score 2652; DB 5; Length 1001;
 Best Local Similarity 90.9%; Pred. No. 8.6e-202;
 Matches 518; Conservative 10; Mismatches 32; Indels 10; Gaps 4;

QY 1 MSPNRWLLIFVSYLMFGAAIYHIEHGEKISRAEQKQAIATNEYLLEELGDKNTT 60
 DB 1 MSPNRWLLIFVSYLMFGAAIYHIEHGEKISRAEQKQAIATNEYLLEELGDKNTT 60
 QY 61 TQDEILQRISDYCDKPVTLPTDYDDTPYTWTFYHAFFAFTVCTVGYGNISPTTAGRM 120
 DB 61 TQDEILQRISDYCDKPVTLPTDYDDTPYTWTFYHAFFAFTVCTVGYGNISPTTAGRM 120
 QY 121 IMIAYSIGIPVNGILFAGLGEYFGRTFEAIYRRYKRYKRMSTDMHYVPPOLGLITWVIA 180
 DB 121 IMIAYSIGIPVNGILFAGLGEYFGRTFEAIYRRYKRYKRMSTDMHYVPPOLGLITWVIA 180

QY 181 LIPGIALFLVPCVGVHLLRELGLSSLSIYSYVYTTTIGFGDYVPTFGANQPKFEGWF 240
 DB 181 LIPGIALFLVPCVGVHLLRELGLSSLSIYSYVYTTTIGFGDYVPTFGANQPKFEGWF 239
 QY 241 VYQIFVWVFIEISGLVYLVMTFITRGLQSKKILAYLEQQLSSNLKATQNRINSVGTVDV 300
 DB 240 VYQIFVWVFIEISGLVYLVMTFITRGLQSKKILAYLEQQLSSNLKATQNRINSVGTVDV 299
 QY 301 GYLRRMLNELYLKVKPVYTDVDTIATLPRNSCPDLSSMYRVEPAPISPKRAFVSVCADM 360
 DB 300 GYLRRMLNELYLKVKPVYTDVDTIATLPRNSCPDLSSMYRVEPAPISPKRAFVSVCADM 359
 QY 361 VQAQREAGMVHANSDDTLTKLDREKTFETAEAYHQTTDLAKVYNALATVKKPPEAQEDA 420
 DB 360 VQAQREAGMVHANSDDTLTKLDREKTFETAEAYHQTTDLAKVYNALATVKKPPEAQEDA 419
 QY 421 ALYGGYHGFSDSOILASEWFSFVNEFTSPRRPRARACSDFNLEAPWQSERPLRSSHNE 480
 DB 420 ALYGGYHGFSDSOILASEWFSFVNEFTSPRRPRARACSDFNLEAPWQSERPLRSSHNE 479
 QY 481 WTWSGDNQIQOEAFAFNQYKGOQRANGAANSTVMVHLEPDALDEEOLRNHRVYVASRSSPCR 540
 DB 480 WTWSGDNQIQOEAFAFNQYKGOQRANGAANSTVMVHLEPDALDEEOLK--QSPGAGRKKFS 537
 QY 541 MCVDDV--CFPSRRSTP-----RRIWSASCP 563
 DB 538 MPDGLRLRFPFOKKRPSQDLERKLSVVVSP 567
 RESULT 2
 Q9JK62 PRELIMINARY; PRT; 502 AA.
 ID AC Q9JK62;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE POTASSIUM CHANNEL TASK2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129 SVJ; TISSUE=KIDNEY;
 RA Roux J., Barhanin J.;
 RT "Mouse two p domain potassium channel TASK2.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF259395; AAF68668.1; -;
 SQ SEQUENCE 502 AA: 55976 MW; E4C7E7CC71B44D95 CRC64;

Query Match 9.4%; Score 308.5; DB 11; Length 502;
 Best Local Similarity 23.8%; Pred. No. 2.8e-16;
 Matches 134; Conservative 86; Mismatches 214; Indels 129; Gaps 21;

QY 4 NRWILLIFVSYLMFGAAIYHIEHGEKISRAEQKQAIATNEYLLEELGDKNTTQD 63
 DB 3 DRGPLLTSAIFVLAIGAAIFEVLEERPHWK-----EAKNYYTQKLLHKEFFCCLSQEGLD 58
 QY 64 EILQRISDYCDKPVTLPTDYDDTPYTWTFYHAFFAFTVCTVGYGNISPTTAGRMIMI 123
 DB 59 KILQVYSDAADQGVAI--TGNQTFNNWNPNAIFAATVITITIGYGNVAPKTPAGRLFCV 116
 QY 124 AVSIVGIPVNGILFAGLGEYFGRTFEAIYRRYKRYKRMSTDMHYVPPOLGLITVIALIP 183
 DB 117 FYGLFGVPLCLTWISALGKFFG-----GRARLQOFLTRRCVSLRKQAITCALFIW 169
 QY 184 GIALFLVPCVGVHLLRELGLSSLSIYSYVYTTTIGFGDYVPTFGANQPKFEGWFVY 243
 DB 170 GVLVHLVIPPV-FVMVTEENWNYIEGLYYSFISTITIGFGDFA--GVNPS---ANYHALY 223
 QY 244 QIFVIVWFVIFSLGYLVNMTF-----ITRGLQSKKILAYLEQQLSS--NLKATQNRINS 294

RN SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=99030343; PubMed=9812978;
 RA Reyes R., Duprat F., Lesage F., Fink M., Salinas M., Farman N.,
 RA Lazdunski M.;
 RT "Cloning and expression of a novel pH-sensitive two pore domain K+
 channel from human kidney.";
 RL J. Biol. Chem. 273:30863-30869(1998).
 CC -1- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING
 POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL
 K+ CONCENTRATIONS.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION
 IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT
 CC EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, QUINIDINE AND EXTERNAL
 ACIDIFICATION.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CHANNELS.
 CC EMBL: AF084830; AAC79458.1; .
 DR MIM: 603493; .
 DR INTERPRO: IPR000099; .
 DR INTERPRO: IPR001622; .
 DR PFAM: PF02034; TWIK_channel; 1.
 DR PRINTS: PR01333; 2POREKCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein. 1
 FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 8 26 POTENTIAL.
 FT DOMAIN 85 112 PORE-FORMING (POTENTIAL).
 FT TRANSMEM 113 133 POTENTIAL.
 FT DOMAIN 134 157 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 158 180 POTENTIAL.
 FT DOMAIN 190 215 PORE-FORMING (POTENTIAL).
 FT TRANSMEM 230 250 POTENTIAL.
 FT DOMAIN 251 325 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 499 AA; 55130 MW; E871A7A4823DDA00 CRC64;

Query Match 9.2%; Score 301; DB 4; Length 499;
 Best Local Similarity 24.6%; Pred. No. 1.1e-15;
 Matches 133; Conservative 93; Mismatches 227; Indels 88; Gaps 23;

QY 4 NRWLLIFVISLMTGAATYYHIEHCEEKISRAEQKQAIAINEYLLELGLDKNTTQD 63
 DB 3 DRGPLTSAIFYLAIGAAIFEELEPHWK----EAKNYYTOKLHLLEKFFCLGQEGLD 58
 QY 64 EILQRSDYCDKPVLTLPPTYDDTPYTWTFYHAFFFAFTVCTGVYGNISPTTFAGRMIMI 123
 DB 59 KILEVVSDAAGQGVAI--TGQNFNNWNNPNAIFAATVITIGYGNVAPKTPAGRLFCV 116
 QY 124 AYSVIGIPVNCILFAGLGEYFGFTFAIVRYKKYKMSMDHVPOLGLITVITVALIP 183
 DB 117 FYGLFGVPLCLTWSALGFFG-----GRAKRLGQFLTGRGVSRLKQAICTVFIIVW 169
 QY 184 GIALFLVPCVGHLLRELGLSSI-SLYTSYVTTTIGFDYVPTFGANQKPEFGGVV 242
 DB 170 GVLVHLVIPPV-FVMYTE-GWNVIEGLYSFIIITIGFDFA--GVNPS----ANYHAL 222
 QY 243 YQIFVAVWFISGLYLVIMTF-----ITRGLQSKKLAYLEQQLSS--NLKANRIW 293
 DB 223 YRVFVELWTVLGLAWLSLFVNNKVSFVEVHKAIKRRRRKESFESSPHSRKALQVK-G 281
 QY 294 SGVTKDGVLRMLNELYLKVKPVYTDV--DIAYVL-----PRNSCP 335
 DB 282 STASKDVNIFS-----FLSKKETYNDLIKQIGKKAMKTSGGGTGPGGLGPGQGGGLP 335
 QY 336 DLSMYRVEPAIPISRKRAFISVCADMYGAOREAGMVHANSDTLTKLDREKTFETAAYHQ 395

Db 336 ALPPSLV-PLVVTGKNRV-PTLEEVSTLRSKGHVSRSPDEEAVARAPEDSSPAPEVFMN 393
 QY 396 TTDLLAKVNALATVKPPPAEQDAALYGYHG--FSDSOILASEWSFVTVNFTSPRRP 453
 Db 394 QLDRISE-----ECEPWDAQD-----YHPLIFQDASITFVNTAGLSDEETS---- 435
 QY 454 RARACSDFNL---EAPRW---OSRPLR-----SSHNEWTWGDNQIQEAFNQYKGGQRA 504
 Db 436 --KSSLEDNLAGEESPQGAERAKAPLNMGEFSSSESTFTSTESLSVPYEQLMNEYNKA 493
 QY 505 N 505
 Db 494 N 494
 RESULT 5
 P97438 PRELIMINARY; PRT; 411 AA.
 ID P97438
 AC P97438; 01-MAY-1997 (TEMBLrel. 03, Created)
 DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
 DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
 DE OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-1 (TWO-PORE
 POTASSIUM CHANNEL TPKC1) (TREK-1 K+ CHANNEL SUBUNIT).
 GN KCNK2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE=BRNIN;
 RX MEDLINE=97157476; PubMed=9003761;
 RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
 RA Lazdunski M.;
 RT "Cloning, functional expression and brain localization of a novel
 unconventional outward rectifier K+ channel.";
 RL EMBO J. 15:6854-6862(1996).
 RN [2]
 RP REVISIONS.
 RC TISSUE=BRNIN;
 RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
 RA Lazdunski M.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP ACTIVATION.
 RX MEDLINE=99254548; PubMed=10321245;
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
 RT "Inhalational anesthetics activate two-pore-domain background K+
 channels.";
 RL Nat. Neurosci. 2:422-426(1999).
 CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
 DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
 LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
 HIPPOCAMPUS AND CEREBELLUM.
 CC -1- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
 ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
 ISOFLURANE.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CHANNELS.
 CC EMBL: U73488; AAC53005.2; .
 DR MGD: MGI:109366; KCnk2.
 DR INTERPRO: IPR000099; .
 DR INTERPRO: IPR001622; .
 DR PFAM: PF02034; TWIK_channel; 1.
 DR PRINTS: PR01333; 2POREKCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein; phosphorylation.
 FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 47 67 POTENTIAL.


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FT DOMAIN 129 155 PORE-FORMING (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 207 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 208 228 POTENTIAL.
FT DOMAIN 238 268 PORE-FORMING (POTENTIAL).
FT TRANSMEM 273 293 POTENTIAL.
FT TRANSMEM 294 311 POTENTIAL.
FT DOMAIN 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY.
FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 300 300 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 303 303 PHOSPHORYLATION (BY CAM-KINASE II) (POTENTIAL).
FT MOD_RES 328 328 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 333 333 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 345 345 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 351 351 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 411 AA; 45297 MW; 8F976DDDD103EFA05 CRC64;

Query Match
Best Local Similarity 9.1%; Score 299.5; DB 11; Length 411;
Matches 110; Conservative 72; Mismatches 151; Indels 95; Gaps 18;

Qy 9 LLFIYISVLMFGAALYYHIEGEEKISRAEQKQAIAINEYLLELGDKNNTTQDEILQR 68
Db 50 IFLVVVLYLIIGAAYVFAKALEQPQE---ISQRTTIVIOKQTFIAQHACVNSTELDELIOQ 105
Qy 69 ISDYCDKPVTLPTTDDPTPTWTFYHAFFAFTVCSTGVGNISPTTFAGRMIMTAYSVI 128
Db 106 IVAAINAGIILPLGNSNQVSHWDLGSSFFAGTIVTTIGFNGISPTREGKIFCIYIALL 165
Qy 129 GIPVNGILFAG---LGEYFGRTFAIYRYKKYKMSDMHYVPPQLGLITVTVIALIPG 184
Db 166 GIPLFGFLAGVDGLGTIFGKIAKVEDTFIKWNV-----QTKIRIISTIIIFL-G 218
Qy 185 TALFLVLPVCGVHLLREL-GLSSI-SLYSYVYTTTTIGFDYVPTFGANQPKFGGFWV 242
Db 219 CVLFVALPAV---IFKHIEGNSALDAIVFVITLTIGFDYVA-----GSDIE 265
Qy 243 YQIFV-IWVF--IFSLGYLWIMTFITRGLQ--SKKLAYLEQQLSMLKATQNRWISGV 296
Db 266 YLDFTKPVVWFILVGLAYFAVLAWSMIGDLRVISKK-----TKEEVGFRAHAAEWTANV 321
Qy 297 TKDVGYLRLMNELYLKVPVYTDVDTLAYTLPRNSCPDLSMYRVEPAPISKRRAFSV 356
Db 322 TAEFKETRRRLS-----VEIYDKFQRAISV-----RRKLS- 351
Qy 357 CADMYGAOREAGMVHANSDDTLTKLDREKTFETABAYHOTDILLAKVYNALATVPPPAE 416
Db 352 -AELAG-----NINQELTPCRR-----TLNVHLTSE-----REVLPPLLK 386
Qy 417 QEDAAIYG 424
Db 387 AESIYVNG 394

RESULT 6
ID 095069 PRELIMINARY; PRT; 426 AA.
AC 095069; Q9UNE3;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DE 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-1 (TWO-PORE POTASSIUM CHANNEL TPKC1) (TREK-1 K+ CHANNEL SUBUNIT).
GN KCNK2 OR TREK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+ channels.";
RL Nat. Neurosci. 2:422-426(1999).
RN [2]
RX SEQUENCE FROM N.A.
RX TISSUE=BRAIN;
RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS CHLOROFORM, HALOTHANE AND ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
DR EMBL; AF129399; AAD47569.1; -.
DR EMBL; AF004711; AAD01203.1; -.
DR MIN; 603219; -.
DR INTERPRO; IPR000099; -.
DR INTERPRO; IPR001622; -.
DR PFAM; PF02034; TWIK_channel; 1.
DR PRINTS; PR01333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein; Phosphorylation.
FT DOMAIN 1 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 82 POTENTIAL.
FT DOMAIN 144 170 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 172 192 POTENTIAL.
FT DOMAIN 193 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 244 POTENTIAL.
FT DOMAIN 253 283 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 288 308 POTENTIAL.
FT DOMAIN 309 426 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 378 426 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY (BY SIMILARITY).
FT DOMAIN 354 426 REQUIRED FOR BASAL CHANNEL ACTIVITY (BY SIMILARITY).
FT MOD_RES 38 38 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 315 315 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 318 318 PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT MOD_RES 343 343 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 348 348 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 360 360 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 366 366 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 2 16 MISSING (IN REF. 2).
FT CONFLICT 309 311 RLV -> DML (IN REF. 2).
FT CONFLICT 391 391 S -> N (IN REF. 2).
FT CONFLICT 411 411 A -> T (IN REF. 2).
SQ SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009F4E CRC64;

Query Match
Best Local Similarity 9.0%; Score 295.5; DB 4; Length 426;
Matches 102; Conservative 76; Mismatches 168; Indels 65; Gaps 15;

Qy 9 LLFIYISVLMFGAALYYHIEGEEKISRAEQKQAIAINEYLLELGDKNNTTQDEILQR 68
Db 65 IFLVVVLYLIIGAAYVFAKALEQPHE---ISQRTTIVIOKQTFISQHSVCNSTELDELIOQ 120
Qy 69 ISDYCDKPVTLPTTDDPTPTWTFYHAFFAFTVCSTGVGNISPTTFAGRMIMTAYSVI 128
Db 121 IVAAINAGIILPLGNTSNQISHWDLGSSFFAGTIVTTIGFNGISPTREGKIFCIYIALL 180
Qy 129 GIPVNGILFAG---LGEYFGRTFAIYRYKKYKMSDMHYVPPQLGLITVTVIALIPG 184
Db 181 GIPLFGFLAGVDGLGTIFGKIAKVEDTFIKWNV-----QTKIRIISTIIIFL-G 233
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RESULT 9
Q9NYG8 PRELIMINARY; PRT; 419 AA.
AC Q9NYG8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE TANDEM PORE DOMAIN POTASSIUM CHANNEL TRAAK.
GN KCKN4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=FRONTAL LOBE;
RC Gray A.T.;
RA "Assignment of KCKN4 encoding the human potassium channel TRAAK to
RT chromosome 11."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF247042; AAF64062.1;
KW Ionic channel.
SQ SEQUENCE 419 AA; 45189 MW; E7CE8E57A35C4FBF CRC64;

Query Match 8.7%; Score 286; DB 4; Length 419;
Best Local Similarity 27.9%; Pred. No. 1.3e-14;
Matches 89; Conservative 57; Mismatches 115; Indels 58; Gaps 11;

QY 7 ILLIFISYLMFGAAIYVHIEGEEKISRAEORAKAIAINEYLLEELGDKNTTQDEIL 66
DB 33 LALLLVLLVYSGALVFRALQEPHE-----QQAQRELGEVREKFLRAHPCVSDQELG 85
QY 67 QRISDYCD-----KPVTLPPYDDTPYTWTFYHAFFFAFTVCSVGYGNISPTTFAGM 120
DB 86 LLIKEVADALGGADPET-NSTSNSSHSADWLGSAFFSGTITITIGYGNVALRTDAGRL 144
QY 121 IMIAYSVIGIPVNGILFAGLGEVFGT-----PEAIYRYKKYKMSDMHYVPPOLGL 173
DB 145 FCIFALVGIPIFGILLAGVDRGLSSLRHGTHIEAIFLKW-----HVPPELV 194
QY 174 ITTVIALIPGIALFLVPCVGVHLLRELGLSISLYSYVTTTIGFGDYVPTFGANQP 233
DB 195 VLSAMFLFLIGCLLFLVLTPTF-VFCYMEDWSKLEAIYFIVITLTVFGGDYVA--CADPR 251
QY 234 KEEGGFVYVQIFVIVWFIFSLGVLVIMTFTIRGLQ-----SKKLAYLEQQLSSNLKA 287
DB 252 QD-----SPAYQPLVWFVILLGLAYFASVLTITIGNLWLVVSVRRTRAEVMGLTAQAAS----- 303
QY 288 TQNRISWG-----VTKDVG 301
DB 304 -----WTGIVTARVTOAG 317

RESULT 10
Q20673 PRELIMINARY; PRT; 551 AA.
AC Q20673; Q20674;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE HYPOTHETICAL 63.2 KDA PROTEIN F52B4.4 IN CHROMOSOME X.
GN F52B4.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Martin J.;
```

Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

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RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U56964; AAB54033.1;
DR INTERPRO; IPR001622;
KW Hypothetical protein.
SQ SEQUENCE 551 AA; 63172 MW; 0C21DF70BC6A1F43 CRC64;
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Query Match 8.1%; Score 264.5; DB 5; Length 551;

Best Local Similarity 23.3%; Pred. No. 1e-12;

Matches 151; Conservative 78; Mismatches 234; Indels 185; Gaps 33;

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QY 9 LLIFISYLMFGAAIYVHIEGEEKISRAEORAKAIAINEYLLEEL--GDKNTTQD 63
DB 25 LMLVLVLYSFLGGFIIDRIETNAHAEMKNERINRTACVS---QILHSIHRWSHNOHKV 81
QY 64 EILQRISDYCDKPVTLPPYDDTPYTWTFYHAFFFAFTVCSVGYGNISPTTFAGMIMI 123
DB 82 QYAEDIAAD-CFEP-----EKDERSEMNVATLVGFGIVTLGYNRIAPITVYGRMFCI 134
QY 124 AYSVIGIPVNGILFAGLGEYFG-----RTFEAIYRYKK-----YKMSDMHY 166
DB 135 VYIGICGIPVTMIITIANVGOYLVNFGADSRKKIEA-YRQORMSKASLAGKIYKES---- 189
QY 167 VPPOLGLITTVIALIPGIALFLVPCVGVHLL-----RELGLSSISLYSYVTTTIGFG 222
DB 190 -----IQVTSIAL---LCVFLIYVAVGALLPLLNGELDFFN-GLYFNFLCLTAIDFG 238
QY 223 DVYPTFGANQPKFEGWVYVQIFVIVWFIFSLGVLVIMTFTIRGLQSKKLAYLQOOLS 282
DB 239 QLVV-----IRVELLPITFLYVVCIGLAITIAINIGSEYMKKLHYWKKMK 284
QY 283 SNLKATQNRISWGTVKDVGYLRRMLNELYLKVKPVYTDVIAITLPRNSCPDLSMYRV 342
DB 285 N---AAQTRIVFGGK-----TLKVR-----DLCHAV--GKKC-----GV 313
QY 343 EPAPISRRKRAFSVCAQMGVQAQREAGMVHANSDDTLTKLDREKTFETAAYHGTDTLLAK 402
DB 314 EP-----GMDA---LDLENV-VERTIAMQEGREPPELDNDE 346
QY 403 VYNALATVPPPAEQEDAALYGGYHGFSQILASWSFSFVNEFTSPRRPRARACSDFN 462
DB 347 -----PPEP-----SPRSIIHSCSTEPSNPPMSPSPREDHFFIFK 384
QY 463 LEAPRWQSERPL-----RSSHNEWTWSDNQIQE-AFNORYKQGOQRAN----- 505
DB 385 MDAPAPRSPPLPAYELDIKKPIFOALSNEFM---NQAQEKLFNDLDTFQIEINTELV 440
QY 506 -GAANSTMVHLEPDALAEQLRNHRVPV---ASRSPCMWCDVCFPSRRS-----TPRR 556
DB 441 EDHKESVIIIEPPATFEDMTIQHSLCEDYEREKVPKR-----FREKKEMYGRDPRK 494
QY 557 INSA-SCPWSRYPRVSRKPKDPRTTSTRSRPPVNPICATDAVRH 603
DB 495 LYETQOEWDRLERLSD-RKHGPRKSVLNLSNCSPPERSV-SPSPIRH 540
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RESULT 11

Q76789

ID Q76789 PRELIMINARY; PRT; 555 AA.

AC Q76789;

DT 01-NOV-1998 (Tremblrel. 08, Created)

DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)

DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)

DE POTASSIUM CHANNEL SUBUNIT N2p16.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

```

[1]
RN SEQUENCE FROM N.A.
RA Wang Z.-W., Kunkel M.T., Wei A., Butler A., Salkoff L.;
RT "Analysis of genomic organization of nematode 4Tm potassium
   channels.";
RL Ann. N.Y. Acad. Sci. 0:0-0(1998).
DR EMBL; AF083645; AAC32856.1;
KW INTERPRO: IPR001622;
SQ SEQUENCE 555 AA; 63858 MW; 4D4E0787AEA3008C CRC64;

Query Match      8.1%; Score 264.5; DB 5; Length 555;
Best Local Similarity 23.3%; Pred. No. 1e-12;
Matches 151; Conservative 78; Mismatches 234; Indels 185; Gaps 33;

Qy 9 LLIFVYSVLMFGAAYHYHIE---HGEKISRAEQKQAIANEVLLLEL---GDKNTTTQD 63
Db 29 LLMVLVLSYFGLGFIQDIETNAHAEMKRNERINRTACVS---QILSHIRWSNQTHKV 85
Qy 64 EILQISDYCDKPVTLPTPTDYTFYHAFFFAFTVCSVGYGNISPTTFAGRMIMI 123
Db 86 QYAEADIAD-CFEP-----EKDERSENFTVATLYGFGIVTTLGYNRIAPITYTCRMFCI 138
Qy 124 AYSVIGIPVNGILFAGLGEYFG-----RTFEAIYRYKK-----YKMTDMHY 166
Db 139 VYGICGIPVTMIITANVQYLLNFAAGDSRRKIEA-YRQRRMSKASLAGKTYKESS----- 193
Qy 167 VPPQGLITTVVIALIPGIALFVLPVCGVHLL-----RELGLSSISLYSVVTTTIGFG 222
Db 194 -----IQVTSAL---LCVFLYIVAVGALLPLLNGLDFFN-GLYFNFLCLTAIDFG 242
Qy 223 DYVTFGANQKPEGGWVYVQIFVIMVIFSLGYLVNIMTFITRGLQSKRLAYLEQOLS 282
Db 243 QLVP-----IRVELLPITFLYVCIGLATTIATINIGSEVMKKLHYWGKKM 288
Qy 283 SNLKATQNRHWSGVTQKGVLRMLNELYLKVKPVTDVDIATLPRNSCPDLSMYRV 342
Db 289 N---AAQTRIFWGGK-----TLKVR-----DLLHAV--GKKC-----GV 317
Qy 343 EPAPIPSKRAFSVCADWGAQREAGMVHANSDTLTKLDREKTFETAAYVHQTDLAK 402
Db 318 EP-----GMDA---LDLENV-VERTIAMQEGREPPELUNDE 350
Qy 403 VVNALATVKPPAPQEDAAALGYGHGFSQSQILASEMSFSVTNFTSPRRPRACRACDFN 462
Db 351 -----PPREP-----SPRSIIHSPCSTRPSNPPMSPSPREDHPHFIEK 388
Qy 463 LEAPRWOSERPL-----RSSHNEWTSQDNGQIQE-AFNQRYKQQRAN----- 505
Db 389 MDAPAPRSLPLPAYELDIKKPIQALSNEFM-----NQSQAQKLFNDLDTFQIEINTELV 444
Qy 506 -GAANSTMVHLEDALEQLRNHRVPV-----ASRSSPCRMVCDVCFPSRRS-----TPRR 556
Db 445 EDHKCESVIIIEPPATFEDTQIHSCLVDEYEREEKVPKR-----FREKKEMYGRDPRK 498
Qy 557 IWSA-SCPWSRYPRVSRKRPDPRTTSTTSRRPPVNPICATDAVRH 603
Db 499 LYETQYQEWDRLERLSD-RKHGPRKRSVNLNLSNCSPPSV-SPSPIRH 544

RESULT 12
Q9XU07 PRELIMINARY; PRT; 393 AA.
AC Q9XU07
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DE T28A8.1 PROTEIN.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.

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OX NCBI_TaxID=6239;
RN SEQUENCE FROM N.A.
RA LLOYD C.;
RX MEDLINE=94150718; PubMed=7906398;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
   elegans.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton A., Dear Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lighthouse J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smailson N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
   elegans.";
RL Nature 368:32-38(1994).
DR EMBL; Z92813; CAB07286.1;
DR INTERPRO: IPR001622;
SQ SEQUENCE 393 AA; 45125 MW; C02BE5ED022EBD8 CRC64;

Query Match      8.0%; Score 264; DB 5; Length 393;
Best Local Similarity 24.4%; Pred. No. 6.9e-13;
Matches 75; Conservative 58; Mismatches 120; Indels 54; Gaps 9;

Qy 7 LLILFVYSVLMFGAAYHYHIECEE-----KISRAEQKQAI-----ATNEYL 50
Db 15 VSLIVLSVVTGFGAFLFYQLEQFNEVEVRARNIERNIHKROMIEHLWEMRESGIGQHV 74
Qy 51 LEEGLDKNTTQDEIL-QRISDYCDKPVTLPTPTDYTFYHAFFFAFTVCSVGYG 109
Db 75 VEDLVKVVYDVTTRILFEAFDTHCIGAKHLRPGGEDEYNTWYMTALFFTTLLTTIGY 134
Qy 110 NISPTTFAGRMIMAYSVIGIPVNGILFAGLGEYFGTTFEAIYRYKKY----- 159
Db 135 NLTPVTGRGKLLCILXALFGVPLILITVADIGKFLSENIVQLYTWYRKLREKSKQYSV 194
Qy 160 -MSTDMHYVPPQLGL-----ITVWVIALIPGIAL-FLVLPVCGVHLLRELGLSSISLYS 212
Db 195 ISSKDKNKEGDLNLDHLENYISIPILVAILLSYITFGAVVLSMWEGWDFTS-GEYFS 253
Qy 213 YVTTTIGFGDYVPTFGANQKPEGGWVYVQIFVIMVIFSLGYLVNIMTFITRGLQSK 272
Db 254 FIMTVTGFQSDIVPL-----KREY-----YILDICYIIIGLSITTCIDLV 294
Qy 273 KLAYLEQ 279
Db 295 GIOYIRK 301

RESULT 13
Q9Z2T2 PRELIMINARY; PRT; 336 AA.
AC Q9Z2T2
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DE PUTATIVE POTASSIUM CHANNEL TWIK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
   SEQUENCE FROM N.A.

```

RA Kaczmarek L.K.;
RT "Cloning and localization of rTWIK, a putative potassium channel with
two P domains."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF022819; AAD09336.1; -
DR INTERPRO; IPR000099; -
DR INTERPRO; IPR001622; -
DR INTERPRO; IPR001779; -
DR PFAM; PF02034; TWIK_channel; 1.
DR PRINTS; PR01096; TWIK1CHANNEL.
DR PRINTS; PR01333; 2PORECHANNEL.
KW Ionic channel.
SQ SEQUENCE 336 AA; 38228 MW; 5E78031947D75DE6 CRC64;

Query Match 7.7%; Score 251.5; DB 11; Length 336;
Best Local Similarity 25.7%; Pred. No. 5.4e-12;
Matches 84; Conservative 65; Mismatches 143; Indels 35; Gaps 11;

QY 9 LLIFVISYLMFGAAIYYHIEGEEKISRAEQKAKIAINEYLLEELGDKNTTQDEILOR 68
Db 26 LVLGVLVLLVFGAVFSSVLEPYEDLLRQELRK----LKRRLFEHECLSEPOLQFLGR 81
QY 69 ISDYCDKPVTLPTDPTTFTVTHAFPEFTVCGTGYGNISPTTFAGRMIMIAYSVI 128
Db 82 VLEASNYGVSVLSNASGN-WNWDFTSALFFASTVLTSTTGTHVPLSDGGKAFACIIYSVI 140
QY 129 GIPVNGILFAGLGEYFGRTFEAIYRYRYKMKSTDMHYVPPQLG---ITTVVIALIPO- 184
Db 141 GIPFT-LLF-----LTAVQRTVHVTRRPVLFHIRWGFSKQVVAIVHAVLLGF 189
QY 185 --IAFLVLPVGVHLLRELGLSSISLYSYVTTTTIGDGVVPTFGANQPKFEGWV 242
Db 190 VTVSFFFTIPAAVSVLEDDWNFLSEFYCFSTLSLTGLDGVPGEGVQNK-----FREL 244
QY 243 YQIFVIVWFISL-CYLVIMWF--ITRGLQSKKLAYLEQQLSS---NLKATQNRITWSGV 296
Db 245 YKIGITCYLLGLLGLAMLVVLETFCEHLKFKRMFYVKKDKDEQVHMEHQDLSFSSI 304
QY 297 TKDVGYLRL--RMLNELYLILKVPVYT 321
Db 305 TEOAGLKEEQKNEPFFVASQSPYED 331

RESULT 14
O17935 PRELIMINARY; PRT; 523 AA.
ID O17935
AC O17935; 045977;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE K06B4.12 PROTEIN.
GN K06B4.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd C.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,
RA Craxton M., Dear S., Du Z., Durbin R., Pavello A., Fulten L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smalton N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans."
RL Nature 368:32-38(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z83233; CAB05769.1; -
DR EMBL; AL021175; CAB05769.1; JOINED.
DR EMBL; AL021175; CAA15972.1; -
DR EMBL; Z83233; CAA15972.1; JOINED.
DR INTERPRO; IPR001622; -
DR PRINTS; PR01333; 2PORECHANNEL.
SQ SEQUENCE 523 AA; 59598 MW; 8A0286680561AC48 CRC64;

Query Match 7.5%; Score 247; DB 5; Length 523;
Best Local Similarity 20.8%; Pred. No. 2.3e-11;
Matches 100; Conservative 88; Mismatches 161; Indels 132; Gaps 19;

QY 5 RWILLIFVISYLMFGAAIYYHIEGEEKISRAEQKAKIAINEYLLEELGDKN 58
Db 130 RHIMVALMVLSTIFGAFMFWESRERAVTLRVTNLENLLNLTATN--ITEIVNPN 187
QY 59 TTTQDEILO-RISDYCDKPVTLPTDPTT-----TWTFYHAFPEFTVCGTVC 107
Db 188 TTTTAEAMQVYIREAVVSLMKLEGQYKGYKLEDHGKNWKWTFESAFFFSMNVT 247
QY 108 YGNISPTTFAGRMIMIAYSVIGIPVNGILFAGLGEYF---GRTFEAIYRYRYKMK 163
Db 248 YGSIAPESILGVVLCYGFIFVPTVLTALRDIGQFFLVHLTKLYAQLIQRWREING 307
QY 164 MHYVPPQLGIITVTALIPGIALFLVPCVGVHLLREL-----GLS-SISLYSYVT 215
Db 308 IDVNE-----IIKIPKACILLALLALYAFCTFIHVFDELSGDSGSMVFICFYS 363
QY 216 TTTTIGDGVVPTFGANQPKFEGWVYQIFVIVWFIFSLGVLVMTITFITRGLQSK 275
Db 364 LSTIGLGDIMPNNATFSP-----IISIMFFGMA-----LTKVVRNRTFI 403
QY 276 YLEQQLSSNLKATQNRINSGVTKDVCYLRLMLNELYLKVPVYTDVLIAYLPRNS 335
Db 404 AVENGIFGALTIVENKL-DGIVR-----KGEKMP 431
QY 336 DLSMYRVEPAIPSR--KRAFSVCAQMGVQAGMVAHNSDTDLTKLDREKTFETA 393
Db 432 D---EQQPKALTPQMIQIALSV-EDYGAQRENKNEVMNFT----- 470
QY 394 HOTTDLLAKVYNALATVKPPPAEQDAALYGGYHGSQ-----TLASEWFSFVNE 448
Db 471 -----VRSIATFM-----KSNTDIYG--GFRVQLRRGLMGSDHQMTSSEKT 513
QY 449 S 449
Db 514 S 514

RESULT 15
O08581 PRELIMINARY; PRT; 336 AA.
ID O08581
AC O08581;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE INWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TWIK-1.
GN KCNK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

OM of: US-08-816-011c-2 to: GenEmbl.* out_format : pfs
Date: Mar 17, 2001 7:23 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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-Q/cgnt2_1/USPTO.spool/US08816011/runat_07032001_122538_23508/app_query.fasta_1.686
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QCAPOP=4.500
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
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Search information block:

Query: US-08-816-011c-2

Query length: 618

Database: GenEmbl.*

Database sequences: 1118133

Database length: 1736092196

Search time (sec): 1799.910000

WARN: APPL_compute_dev_space_s: pointers violation: prPtr=5af1716 !

score_list:

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gb_pat1.i26670	+ 3283.00	2583.12	1.0e-135	2441	I26670 Sequence 1 from patent
gb_in3:DMU55321	+ 3165.50	2488.36	1.9e-130	3568	I26670 Sequence 1 from patent
gb_hc95:AC013909	+ 2648.00	2070.27	3.7e-107	21163	I26670 Sequence 1 from patent
gb_in1:AE003484	- 2648.00	2052.01	3.9e-106	314087	I26670 Sequence 1 from patent
gb_ro:AX018705	+ 312.00	254.08	5.4e-06	1794	I26670 Sequence 1 from patent
gb_ro:AX018705	+ 312.00	254.08	5.4e-06	1795	I26670 Sequence 1 from patent
gb_ro:AF259395	+ 310.00	253.68	5.7e-06	1509	I26670 Sequence 1 from patent
gb_pr3:AF084830	+ 305.00	244.04	2.0e-05	3514	I26670 Sequence 1 from patent
gb_pr4:AF279890	+ 300.00	241.82	2.6e-05	2730	I26670 Sequence 1 from patent
gb_ro:MMU73488	+ 299.50	239.60	3.5e-05	3580	I26670 Sequence 1 from patent
gb_ro:AX018706	+ 298.50	242.78	2.3e-05	1993	I26670 Sequence 1 from patent
gb_ro:AX003051	+ 298.50	242.77	2.3e-05	1994	I26670 Sequence 1 from patent
gb_pr4:AF247042	+ 298.50	240.54	3.1e-05	2772	I26670 Sequence 1 from patent
gb_ro:AF196965	+ 295.50	240.91	2.9e-05	1854	I26670 Sequence 1 from patent
gb_pr3:AF004711	+ 295.50	240.05	3.3e-05	2106	I26670 Sequence 1 from patent
gb_pr5:AX003047	+ 292.50	241.25	2.8e-05	1246	I26670 Sequence 1 from patent
gb_pr4:AF171068	+ 292.50	241.21	2.8e-05	1252	I26670 Sequence 1 from patent
gb_pr3:AF129399	+ 291.50	240.52	3.1e-05	1236	I26670 Sequence 1 from patent
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gb_in2:AF083646	+ 245.00	204.85	0.0030	1095	I26670 Sequence 1 from patent
gb_ro:AF031384	+ 244.00	199.73	0.0057	2077	I26670 Sequence 1 from patent
gb_pr3:AF006823	+ 243.00	197.46	0.0077	2590	I26670 Sequence 1 from patent
gb_hc94:AC012766	+ 243.00	180.14	0.0708	33463	I26670 Sequence 1 from patent
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gb_in2:AF083652	+ 241.00	202.40	0.0041	990	I26670 Sequence 1 from patent
gb_ro:AF006824	+ 240.00	197.25	0.0079	1887	I26670 Sequence 1 from patent
gb_ro:AF022821	+ 239.00	201.49	0.0046	897	I26670 Sequence 1 from patent
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gb_pr7:HSU76996	+ 239.00	196.56	0.0086	1860	I26670 Sequence 1 from patent
gb_pr7:HSU33632	+ 239.00	196.48	0.0087	1882	I26670 Sequence 1 from patent
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gb_ro:AB013345	+ 239.00	196.04	0.0092	2009	I26670 Sequence 1 from patent
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gb_on:AF004695	+ 227.50	193.42	0.0129	780	I26670 Sequence 1 from patent
gb_in2:AF083653	+ 211.50	176.64	0.1108	1455	I26670 Sequence 1 from patent

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gb_pr4:AF281302 + 210.50 178.28 0.0898 1017 ! AF281302 Homo sapiens 2p do
gb_pr5:AX020359 + 210.50 173.12 0.1741 2180 ! AX020359 Sequence 1 from Pa
gb_pat1:AF94721 + 210.50 173.12 0.1741 2180 ! AF94721 Sequence 1 from Pate
gb_pr3:AF134149 + 210.50 171.80 0.2061 2649 ! AF134149 Homo sapiens 2-por
seq_name: gb_pat1.i26670
seq_documentation_block:
LOCUS I26670 2441 bp DNA PAT 07-OCT-1996
DEFINITION Sequence 1 from patent US 5559026.
ACCESSION I26670
VERSION I26670.1 GI:1606540
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2441)
AUTHORS Price L.A. and Pausch, M.H.
TITLE Genes encoding a novel family of potassium channels
JOURNAL Patent: US 5559026-A 1 24-SEP-1996;
FEATURES
Location/Qualifiers
source
BASE COUNT 555 a 702 c 665 g 519 t
ORIGIN
alignment_scores:
Quality: 3283.00 Length: 618
Ratio: 5.312 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-08-816-011c-2 x I26670
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190 ATGTCGCCGAATCGATGATCGCTGCTCATCTTACATATCTTACCT 239
17 uMetPheGlyAlaAlaIleTyrTrpHisIleGluHisGlyGluGluLysI 34
240 GATGTTTCGGCGCGGCAATCTATTACCATATTGACGACGCGGAGAGAAGA 289
34 leSerArgAlaGluGlnArgLysAlaGlnIleAlaIleAsnGluTyrLeu 50
290 TATCGCGCGCGGCAACGCGGCAAGCAATTCGAATCAACGAATATCTG 339
51 LeuGluGluLeuGlyAspLysAsnThrThrThrGlnAspGluIleLeuG1 67
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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cerevisiae
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (23), 13256-13261 (1996)
MEDLINE 97075152
REFERENCE 2 (bases 1 to 3568)
AUTHORS Goldstein,S.A.N., Price,L.A., Rosenthal,D.N. and Pausch,M.H.
TITLE Direct Submission
JOURNAL Submitted (17-APR-1996) S.A.N. Goldstein, Pediatrics and Cellular
and Molecular Physiology, Yale University School of Medicine, Boyer
Center for Molecular Medicine, 295 Congress Avenue, New Haven, CT
06536, USA
REFERENCE 3 (bases 1 to 3568)
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AUTHORS Goldstein, S.A.N., Price, L.A., Rosenthal, D.N. and Pausch, M.H.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-1998) S.A.N. Goldstein, Pediatrics and Cellular
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Center for Molecular Medicine, 295 Congress Avenue, New Haven, CT
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REMARK Sequence update by submitter
COMMENT On Oct 29, 1998 this sequence version replaced gi:1666502.
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VERSION AC013909.1 GI:6437426

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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 21163)
AUTHORS Adams,M. and Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10210421 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
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REFERENCE
ADAMS,M.D., CELNIKER,S.E., HOLT,R.A., EVANS,C.A., GOCAYNE,J.D.,
AMANTIDES,P.G., SCHERER,S.E., LI,P.W., HOSKINS,R.A., GALLE,R.F.,
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ANDREWS-PFANNKUCH,C., BALDWIN,D., BALLEW,R.M., BASU,A.,
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Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
Science 287 (5461), 2185-2195 (2000)
20196006
TITLE 2 (bases 1 to 314087)
JOURNAL
AUTHORS Adams,M.D., Celnikier,S.E., Gibbs,R.A., Rubin,G.M. and Venter,J.C.
REFERENCE Direct Submission
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Rockville, MD, USA
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ACCESSION AX018705
VERSION AX018705.1 GI:10042825
KEYWORDS
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ORGANISM Mus sp.
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1 (bases 1 to 1794)
Fink, M., Honore, E., Duprat, F., Lesage, F. and Lazdunski, M.
Novel mechanically sensitive mammalian potassium channel family
activated by polyunsaturated fatty acids and their use particularly
for screening medicines
JOURNAL Patent: WO 9945108-A 10-SEP-1999;

FINK MICHEL (FR); HONORE ERIC (FR); DUPRAT FABRICE (FR); LESAGE
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Fink, M., Lesage, F., Duprat, F., Heurteaux, C., Reyes, R., Fosset, M.
and Lazdunski, M.
A neuronal two P domain K⁺ channel stimulated by arachidonic acid
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DEFINITION Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.
ACCESSION AF084830
VERSION AF084830.1 GI:3925426
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3514)
AUTHORS Reyes,R., Duprat,F., Lesage,F., Fink,M., Salinas,M., Farman,N. and Lazdunski,M.
TITLE Cloning and expression of a novel pH-sensitive two pore domain K+ channel from human kidney
J. Biol. Chem. 273 (47), 30863-30869 (1998)
JOURNAL 99030343
MEDLINE 9812978
REFERENCE 2 (bases 1 to 3514)
AUTHORS Reyes,R., Duprat,F., Lesage,F., Fink,M., Salinas,M., Farman,N. and Lazdunski,M.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-1998) IPCM, CNRS, 660 Route des Lucioles, Sophia Antipolis, Valbonne 06560, France

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mRNA, complete cds.
ACCESSION AF247042
VERSION AF247042.1 GI:7576934
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2772)
AUTHORS Gray, A.T.
TITLE Assignment of KCNK4 encoding the human potassium channel TRAAK to
chromosome 11
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2772)
AUTHORS Gray, A.T.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Anesthesia, Room S 261, UC San Francisco,
513 Parnassus Avenue, San Francisco, CA 94143-0542, USA
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DEFINITION Homo sapiens two-pore potassium channel TPKC1 mRNA, complete cds.

ACCESSION AF004711

VERSION AF004711.1 GI:4101565

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2106)

AUTHORS Price,L.A., Hellings,S.E., Hayashi,J.H. and Pausch,M.H.

TITLE TPKC1

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2106)

AUTHORS Price,L.A., Hellings,S.E., Hayashi,J.H. and Pausch,M.H.

TITLE Direct Submission

JOURNAL Submitted (19-MAY-1997) Cyanamid Agricultural Research Center,

American Cyanamid Company, PO Box 400, Princeton, NJ 08543-0400,

USA

FEATURES

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Quality: 295.50 Length: 411

Ratio: 1.296 Gaps: 15

Percent Similarity: 55.474 Percent Identity: 24.818

alignment_block:

US-08-816-011C-2 x AF004711 ..

Align seg 1/1 to: AF004711 from: 1 to: 2106

9 LeuLeuIlePheTyrIleSerTyrLeuMetPheGlyAlaAlaIleTyrTy 25

.....

346 ATATTCCTGGTGGTTGCTCTATCTGATCATCGGAGCCACCGTGTCAA 395

25 rHisIleGluHisGlyGluGlyLysIleSerArgAlaGluGlnArgLysA 42

.....

396 AGCATTTGGAGCAGCCTCATGAG.....ATTTCACAGAGGACCA 433

42 lagInIleAlaIleAsnGluTyrLeuGluLeuGlyAspLysAsn 58

.....

OM of: US-08-816-011c-2 to: N_Geneseq_36:* out_format : pfs
 Date: Mar 17, 2001 7:55 PM
 About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
 -O=cg2_1/USPTO.spool/US08816011/runat_07032001_122539_23551/app_query.fasta_1.686
 -DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=ring -GAPOP=12.000
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -FGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosome2
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
 -NORM=ext -MINLEN=0 -MAXLEN=200000000
 -USER=US08816011_@CGN1_1_147 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
 -WAIT -THREADS=1

Search information block:

Query: US-08-816-011c-2
 Query length: 618
 Database: N_Geneseq_36:*
 Database sequences: 480022
 Database length: 187831343
 Search time (sec): 90.290000

score_list:

Sequence	Strd Orig	zScore	EScore	Len	! Documentation
/cg2_2/gcgdata/geneseq/NA1996.DAT:T33201			3283.00	4009.66	2441
/cg2_2/gcgdata/geneseq/NA1999.DAT:T10606			312.00	369.82	1794
/cg2_2/gcgdata/geneseq/NA2000.DAT:AL15953			306.00	355.29	5.3e-12
/cg2_2/gcgdata/geneseq/NA2000.DAT:AL15943			301.00	358.08	3.7e-12
/cg2_2/gcgdata/geneseq/NA1999.DAT:T10607			298.50	352.25	7.9e-12
/cg2_2/gcgdata/geneseq/NA1999.DAT:T00004			298.50	352.24	7.9e-12
/cg2_2/gcgdata/geneseq/NA1999.DAT:T00039			292.50	349.43	1.1e-11
/cg2_2/gcgdata/geneseq/NA1999.DAT:T11914			292.50	340.02	3.8e-11
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/cg2_2/gcgdata/geneseq/NA2000.DAT:A27106			286.00	341.68	3.0e-11
/cg2_2/gcgdata/geneseq/NA2000.DAT:T64960			243.00	286.62	3.6e-08
/cg2_2/gcgdata/geneseq/NA1997.DAT:T64960			239.00	279.78	8.5e-08
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/cg2_2/gcgdata/geneseq/NA1999.DAT:T11914			210.50	241.89	1.1e-05
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/cg2_2/gcgdata/geneseq/NA2000.DAT:T46094			210.50	241.29	1.2e-05
/cg2_2/gcgdata/geneseq/NA1996.DAT:T33202			208.50	248.45	4.7e-06
/cg2_2/gcgdata/geneseq/NA1999.DAT:T00004			169.50	211.71	0.0005
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/cg2_2/gcgdata/geneseq/NA1998.DAT:T13572			143.00	151.42	1.20
/cg2_2/gcgdata/geneseq/NA1999.DAT:T23031			141.50	147.81	1.91
/cg2_2/gcgdata/geneseq/NA2000.DAT:T58965			131.00	146.79	2.18
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/cg2_2/gcgdata/geneseq/NA1999.DAT:T28369			125.50	135.20	9.64
/cg2_2/gcgdata/geneseq/NA1999.DAT:T28367			125.50	135.00	9.90
/cg2_2/gcgdata/geneseq/NA1995.DAT:T81328			125.50	127.26	26.73
/cg2_2/gcgdata/geneseq/NA1999.DAT:T28371			125.50	130.50	63.55
/cg2_2/gcgdata/geneseq/NA1987.DAT:T70566			125.00	135.38	9.43
/cg2_2/gcgdata/geneseq/NA1997.DAT:T85474			124.50	128.43	23.00
/cg2_2/gcgdata/geneseq/NA1998.DAT:T16307			124.50	128.43	23.00
/cg2_2/gcgdata/geneseq/NA2000.DAT:T494761			124.50	127.50	25.92
/cg2_2/gcgdata/geneseq/NA1998.DAT:T16345			124.50	127.44	26.08
/cg2_2/gcgdata/geneseq/NA1998.DAT:T36085			124.00	141.69	4.20
/cg2_2/gcgdata/geneseq/NA1997.DAT:T73334			123.50	131.54	15.43

/cg2_2/gcgdata/geneseq/NA1997.DAT:T78508 + 123.00 107.09 355.04 44377
 /cg2_2/gcgdata/geneseq/NA1997.DAT:T80414 + 123.00 107.09 355.04 44377
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 /cg2_2/gcgdata/geneseq/NA1997.DAT:T61016 + 122.00 109.64 255.82 30001
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seq_name: /cg2_2/gcgdata/geneseq/NA1996.DAT:T33201

seq_documentation_block:

ID T33201 standard; cDNA; 2441 BP.
 AC T33201;
 XX
 DT 16-OCT-1996 (first entry)
 XX
 DE DmORF1 potassium channel gene.
 XX
 KW DmORF1; potassium channel; fruitfly; polyadenylation site;
 KW potassium dependence; Saccharomyces cerevisiae; potassium-agonist;
 KW potassium-antagonist; drug screening; insecticide; cardiac disorder;
 KW ss.
 XX
 OS Drosophila melanogaster.

EH Key Location/Qualifiers
 FT CDS 190..2046

FT /*tag= a
 FT /product= Potassium channel DmORF1 protein
 FT polyA_signal 2093..2098
 FT /*tag= b

XX WO9613520-A1.

XX 09-MAY-1996.

XX 25-OCT-1995; 95WO-US14364.

XX 31-OCT-1994; 94US-0332312.

XX (AMCY) AMERICAN CYANAMID CO.

XX Pausch MH, Price LA;

XX WPI; 1996-239450/24.

XX P-PSDB; R97984.

Potassium channel genes from *Drosophila melanogaster* and *Caenorhabditis elegans* - useful in assaying substances to determine effects on cell growth, and in inhibiting nematode and insect pests

Claim 11; Page 34-37; 79pp; English.

The sequence encodes potassium channel DmORF1 protein from *Drosophila melanogaster*, with 2 pore-forming domains between transmembrane helix domains. The sequence has been isolated by complementation of the potassium-dependent phenotype of *Saccharomyces cerevisiae* Cvi62 (trk1-delta) on low-potassium medium. The 5'-untranslated sequence contains long poly-A and poly-T tracts not likely to be found in protein coding regions. A consensus polyadenylation site is found in the 3'-untranslated sequence. Primers T33205-06 may be used to amplify the open reading frame, for cloning and expression in *Xenopus laevis* oocytes and assaying induced potassium currents. The DNA may be inserted in a vector and expressed in a host cell to assay substances to determine effects on cell growth. Potassium-agonists or potassium-antagonists identified by this method may be used as insecticides or in therapy of cardiac disorders, etc.

Sequence 2441 BP; 555 A; 702 C; 665 G; 519 T; 0 other;

alignment_scores:

Quality: 3283.00 Length: 618

Ratio: 5.312 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-08-816-011c-2 x T33201 ..
Align seg 1/1 to: T33201 from: 1 to: 2441

1 MetSerProAsnArgTrpIleLeuLeuLeuIlePheTyrIleSerTyrLe 17
190 ATGTGCGCGCAATCGATGATCTGCTGCTCATCTTCTACATATCCTACCT 239
17 uMetPheGlyAlaIleTyrTyrHisIleGluHisGlyGluLysI 34
240 GATGTTGGGGCGGCAATCTATTACCATATTGAGCACGGCGAGGAGAAGA 289
34 leSerArgAlaGluGlnArgIysAlaGlnIleAlaIleAsnGluTyrLeu 50
290 TATCGCGCGCGCAACAGCGCAAGCGCAAAATTGCAATCAACGAATATCTG 339
51 LeuGluGluLeuGlyAspLysAsnThrThrGlnAspGluIleLeuG1 67
340 CTGGAGGAGCTGGCGCAACAAATACGACACACAGGATGAGATTCATTCA 389
67 nArgIleSerAspTyrCysAspLysProValThrLeuProThrTyrA 84
390 ACGGATCTCGGATTACTGTGCAAAACCGTTTACATTGGCCGCGACATATG 439
84 spAspThrProTyrThrThrPheTyrHisAlaPhePheAlaPhe 100
440 ATGATACGCCCTACACGTGGACCTTCTACCATGGCTTCTTCTGCGCTTC 489
101 ThrValCysSerThrValGlyTyrGlyAsnIleSerProThrThrPheAl 117
490 ACCGTTTCTCCACGGTGGGATATGGGAATATATCGCAACCACTTCGC 539
117 aGlyArgMetIleMetIleAlaTyrSerValIleGlyIleProValAsnG 134
540 CGGACGGATGATCATGATCGCGTATTTCGGTGATTGGCATCCCGCTCAATG 589
134 lyIleLeuPheAlaGlyLeuGlyGluTyrPheGlyArgThrPheGluAla 150
590 GTATCTCTTTGGCGGCTCGGGAATACTTTGGACGTACGTTTGAAGCG 639
151 IleTyrArgTyrLysLysTyrLysMetSerThrAspMetHisTyrVa 167
640 ATCTACACACCTCAAAAACTACAAGATGTCACGGATATGCATATGT 689
167 lProProGlnLeuGlyLeuIleThrThrValIleAlaLeuIleProG 184
690 CCCGCGCAGCTGGGATTGATCACCACCGTGGTGTGTTGCCCTGATTCGG 739
184 lyIleAlaLeuPheLeuValLeuProCysValGlyValHisLeuLeuArg 200
740 GAATAGCTCTCTTCGTGTGTCGCCGCGGGGTGTTCACCTACTTCGA 789
201 GluLeuGlyLeuSerSerIleSerLeuTyrTyrSerTyrValThrThrTh 217
790 GAACCTGGSCCTATCTTCATCTCGCTGTACTACAGCTATGTGACCACCA 839
217 rThrIleGlyPheGlyAspTyrValProThrPheGlyAlaAsnGlnProL 234
840 AACAAATTGGATTTCGCTACTATGTGCCACACATTTGGAGCCCAACAGCCCA 889
234 ysGluPheGlyGlyTrpPheValValTyrGlnIlePheValIleValTrp 250
890 AGGAGTTCCGGCGGCTGGTGTGCTGTATCAGATCTTTGGTATCGTGTGG 939
251 PheIlePheSerLeuGlyTyrLeuValMetIleMetThrPheIleThrAr 267
940 TTATCTTCTCGCTGGGATATCTTGTGATGATCATGACATTTATCACTCG 989
267 gGlyLeuGlnSerLysLysLeuAlaTyrLeuGluGlnLeuSerSerA 284

990 GGGCTCCAGACGAAGAGCTGGCATACCTGGAGCAGCAGTTGCTCTCCA 1039
284 snLeuLysAlaThrGlnAsnArgIleTrpSerGlyValThrLysAspVal 300
1040 ACCTGAAGGCCACACAGAAATCGCATCTGGTCTGGCGTCCACCAAGATGTG 1089
301 GlyTyrLeuArgArgMetLeuAsnGluLeuTyrIleLeuLysValLysPr 317
1090 GGCTACCTCCGCGCAATCTCAACGAGCTGTACATCTCTCAAGTGAAGCC 1139
317 oValTyrThrAspValAspIleAlaTyrThrLeuProArgSerAsnSerC 334
1140 TGTGTACACCGATGTAGATATCGCTACACACTGCCACGTTTCCAATCGT 1189
334 ysProAspLeuSerMetTyrArgValGluProAlaProIleProSerArg 350
1190 GTCCGGATCTGAGCATGTACCGCTGGAGCGGCTCCCATTTCCAGCGGG 1239
351 LysArgAlaPheSerValCysAlaAspMetValGlyAlaGlnArgGluAl 367
1240 AAGAGGCGATTCTCGGTGCGCGCGACATGTTGGCGCCCAAGGGAGGC 1289
367 aGlyMetValHisAlaAsnSerAspThrAspLeuThrLysLeuAspArg 384
1290 GGGCATGTACACGCCAATTCGGATACGGATCTAACCAAACTGGATCGCG 1339
384 luLysThrPheGluThrAlaGluAlaTyrHisGlnThrThrAspLeuLeu 400
1340 AGAAGACATTCGAGACGGCGGAGGCTACCAACAGACCGCATTTGCTG 1389
401 AlaLysValValAsnAlaLeuAlaThrValLysProProAlaGluG1 417
1390 GCCAAGTGGTCAACGCACCTGGCCACCGTGAAGCCACCGCGCGGAACA 1439
417 nGluAspAlaAlaLeuTyrGlyTyrHisGlyPheSerAspSerGlnI 434
1440 GGAAGATCGCGCTCTCTATGTTGGCTATCATGGCTTCTCCGACTCCAGA 1489
434 leLeuAlaSerGluTrpSerPheSerThrValAsnGluPheThrSerPro 450
1490 TCTTGGCCAGCAATGGTGTCTCGACGGTCAACGAGTTTCACATCACCG 1539
451 ArgArgProArgAlaArgAlaCysSerAspPheAsnLeuGluAlaProAr 467
1540 CGACGTCCAAGAGCACCTGGCTGCTCCGATTTCAATCTGGAGGCACTCG 1589
467 gTrpGlnSerGluArgProLeuArgSerSerHisAsnGluTrpThrTrpS 484
1590 CTGGCAGAGCGAGAGCGCACTGCTTTCGAGCCACACGAATGGACATGGA 1639
484 erGlyAspAsnGlnGlnIleGlnGluAlaPheAsnGlnArgTyrLysGly 500
1640 GCGGCGCAACACAGCAGATCCAGGAGCATTCACACCGCTACAGGGA 1689
501 GlnGlnArgAlaAsnGlyAlaAlaAsnSerThrMetValHisLeuGluPr 517
1690 CAGCAGCTGCCAACGAGCAGCAACTCGACCATGCTCCATCTGGAGCC 1739
517 oAspAlaLeuGluGlnLeuArgAsnAsnHisArgValProValAlas 534
1740 GGATGCTTTGGAGGAGCAGCTGAGAAACAATACCGGGTGGCGTCCGCT 1789
534 erArgSerSerProCysArgMetValCysAspValCysPheProSerArg 550
1790 CAGAAGTCTTCCATGCCGATGCTGCGACGCTCTGTTTCCCTTCCAGA 1839
551 ArgSerThrProArgIleTrpSerAlaSerCysProTrpSerArgTy 567
1840 AGAAGCACCCCTCGCAGGATCTGGAGCGCAAGTTGTCGGTGGTCTCGTA 1889
567 rProArgValSerSerArgArgLysProAspProArgTrpThrThrS 584

```

1890 CCGAGGGTGTCTATCTCGCAGGAAGCCAGATCCCGCTGGACTACTACAT 1939
584 erThrArgSerArgProValAsnProIleCysAlaThrAspAla 600
1940 CAACACGGTACACGGCGCTCCAGTCAATCTATTGCGCAACGGACGCG 1989
601 ValArgHisArgProSerAsnArgMetAlaAlaAlaAlaAlaAla 617
1990 GTCCGCCACCGCCCTTCGAATCAATGGCAGCTTGCCACGCGCGCGGC 2039
617 agly 618
2040 GGC 2043

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seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NAL1999.DAT:Z10606

seq_documentation_block:

ID Z10606 standard; CDNA; 1794 BP.

AC Z10606;

DT 18-NOV-1999 (first entry)

DE CDNA encoding a mechanically sensitive potassium channel protein TRAAK.

KW Mechanically sensitive potassium channel protein; TRAAK;

KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;

KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;

KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;

KW muscular disease; ds.

OS Mus sp.

XX FH Key Location/Qualifiers

FT CDS 284..1480

FT /*tag= a

XX PN W09945108-A2.

XX PD 10-SEP-1999.

XX PF 23-FEB-1999; 99WO-FR00404.

XX PR 05-MAR-1998; 98FR-0002725.

XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;

XX DR WPI; 1999-551038/46.

XX DR P-PSDB; Y30647.

XX PT New mechanically sensitive potassium channel, used to screen for specific modulators, potential therapeutic agents for heart and nervous system disorders

XX PS Claim 6; Fig 1; 40pp; French.

XX CC The present sequence encodes a mechanically sensitive potassium channel protein designated TRAAK. The protein is activated by polyunsaturated fatty acids, particularly arachidonic acid, and by riluzole. The protein is used to screen for specific modulators which are useful for treating or preventing diseases of the heart and nervous systems in humans and animals, e.g. epilepsy, cardiovascular disease (arrhythmia), neurodegeneration (particularly where associated with ischemia or anoxia), abnormalities of hormone secretion and muscular disease. The protein itself may be used to treat these diseases. Antibodies specific for the protein are used to detect it in tissues, also as therapeutic inhibitors or activators.

XX SQ Sequence 1794 BP; 348 A; 574 C; 494 G; 378 T; 0 other;

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alignment_scores:
  Quality: 312.00      Length: 388
  Ratio: 1.625        Gaps: 14
  Percent Similarity: 49.485  Percent Identity: 26.804

alignment_block:
US-08-816-011C-2 x Z10606

Align seg 1/1 to: Z10606 from: 1 to: 1794

7  IleLeuLeuLeuIlePheTyrrilleSerTyrrLeuMetPheGlyAlaAlaI 23
   ::  |||||  ::  ::  |||||  ::  |||||  ::  |||||  ::
302 CTGGCTCTGCTGGCACTGGTGTCTGCTTTACTTGTGTCTGGGCTCTAGT 351

23 eTyrrTyrrHisIleGlu..... 28
   ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
352 GTTCCAGGCTCTGGAGCAGCTCACGAGCAGCAGGCTCAGAGAAAATGG 401

29  ..HisGlyGluGluLysIleSerArgAlaGluGlnArgLysAlaGlnIle 44
   |||||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
402 ATCATGGCCGAGACCACTTCTGAGGACCATCCCTGTGTGAGCCAGAG 451

45 AlaIleAsnGluTyrr.....LeuLeuGluGluLeuGlyAspLysAs 58
   ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
452 AGCCTGGAGGATTCATCAAGCTCTGTTGAAGCCCTGGAGGGGCG... 499

58 nThrThrThrGlnAspGluLeuGlnArgIleSerAspTyrrCysAspL 75
   ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
500 .....GCAA 503

75 ysProValThrLeuProThrTyrrAspAspThrProTyrrThrTrpThr 91
   ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
504 ACCCAGAACCCAGCTGGACCAATAGCAGCAACACCCTCATCAGCTTGAAC 553

92 PheTyrrHisAlaPhePheAlaPheThrValCysSerThrValGlyTy 108
   ::  |||||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
554 CTGGGCGAGCGCTTCTTTCTCGGGGACCATCATCATTACATCGGCTA 603

108 rGlyAsnIleSerProThrThrPheAlaGlyArgMetIleAlaIle 125
   |||||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
604 TGCAATATAGTCTTACACACAGATCGGGGCGTCTCTTTTGTATCTCT 653

125 yrSerValIleGlyIleProValAsnGlyIleLeuPheAlaGlyLeuGly 141
   |||||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
654 ATGCACTGGTGGGATCCCACTGTTCGGGATGCTGCTGGCGGAGTCGGG 703

142 GlutyrPheGlyArgThr.....PheGluAlaIle 151
   ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
704 GACCGCTGGCTCTCTGCGCGGGGCGATCGGCCACATCGAAGCAAT 753

151 eTyrrArgTyrrLysTyrrLysMetSerThrAspMethIleTyrrValP 168
   ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
754 CTCTTGAAGTGG.....CATGTGC 773

168 roProGlnLeuGlyLeuIleThrThrValIleAlaLeuIleProGly 184
   |||||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
774 CACCGGGGCTGGTGAAGTCTGTCCGAGTCTCTCTCTGCTGATCGGC 823

185 IleAlaLeuPheLeuValLeuProCysValGlyValHisLeuLeuArg 201
   |||||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
824 TGCTGCTCTTTCTCTCACTCTCTACCTTC....CTGTTCTCTACATGGA 870

201 uLeuGlyLeuSerSerIleSerLeuTyrrSerTyrrValThrThrThr 218
   ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
871 GAGCTGGAGCAAGTTAGAACCCATCTACTTTGTATAGTGACTCTCACCA 920

218 hrIleGlyPheGlyAspTyrrValProThrPheGlyAlaAsnGlnPro 234
   |||||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
921 CTGTAGGCTTTGGCGATTATGTACCCGGGATGGCCCGGCGAGAACTCT 970

235 GluPheGlyGlyTrpPheValValTyrrGlnIlePheValIleValTrp 251
   ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
971 CCA.....GCCTACACCGCTGTGTGGTCTCTGGAT 1002

```


nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury; systemic cytokine damage; tissue differentiation; contraceptive; stroke; coagulation disorder; myocardial infarction; inflammatory condition; septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour; nephritis; therapy; ss.

Homo sapiens.

WO200005367-A2.

03-FEB-2000.

22-JUL-1999; 99WO-JP03929.

24-JUL-1998; 98JP-0208820.

07-AUG-1998; 98JP-0224105.

25-AUG-1998; 98JP-0238116.

09-SEP-1998; 98JP-0254736.

29-SEP-1998; 98JP-0275505.

(SAGA) SAGAMI CHEM RES CENT.
(PROT-) PROTEGENE INC.

Kato S, Kimura T;

WPI; 2000-182694/16.

P-PSDB; Y94875.

Novel human proteins having hydrophobic domains useful for treating osteoporosis, Alzheimer's disease, Parkinson's disease, asthma, multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -

Claim 3; Page 252-253; 351pp; English.

This sequence encodes a human protein of the invention, which has hydrophobic domains. The DNA sequences can be used as a probe or as a genetic marker. The protein can also be used as a marker, and to identify potential genetic disorders. The DNA and protein can also be used as nutritional sources or supplements. The protein exhibits cytokine, cell proliferation, cell differentiation activities and induces production of other cytokines in certain cell populations. The protein also exhibits immune stimulating or immune suppressing activity. It can be used in the treatment of various immune deficiencies and disorders, and to treat infectious diseases caused by viral, bacterial, fungal or other infections. The protein is also used for treating autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid arthritis. It is also useful in the treatment of allergic reactions and conditions such as asthma, and in immune suppression after organ transplantation. The protein is useful in regulation of haematopoiesis and consequently in the treatment of myeloid or lymphoid cell deficiencies. It is also used in compositions for tissue growth or regeneration. The protein is also used in the treatment of osteoporosis or osteoarthritis and in the treatment of periodontal disease and other tooth repair processes. The protein is used in the treatment of nervous system disorders such as Alzheimer's disease, Parkinson's disease, and Huntington's disease. They are useful for protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage. They are also used for promoting or inhibiting tissue differentiation. They are also used as contraceptives since they exhibit activin or inhibin related activities and as a fertility inducing therapeutic. They are used for treating various coagulation disorders and in treatment and prevention of conditions resulting from coagulation activities e.g. myocardial infarction or stroke. They also acts as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. They are used to treat inflammatory conditions such as septic shock, sepsis, ischaemia reperfusion injury, arthritis, and nephritis. They can be used to prevent tumours.

Sequence 1497 BP; 328 A; 447 C; 438 G; 284 T; 0 other;

alignment_scores: Quality: 301.00 Length: 541
 Ratio: 1.020 Gaps: 23
Percent Similarity: 54.529 Percent Identity: 24.584

alignment_block:
US-08-816-011c-2 x A15943

Align seg 1/1 to: A15943 from: 1 to: 1497

4 AsnArgTrpIleLeuLeuLeuIlePheTyrIleSerTyrLeuMetPheG1 20
 :::||||| ||||| ||| ||||| ::|||
7 GACCGGGCCCTCTGCATCACCCTCGGCCATCATCTTCTACCTGGCCATCG 56
 ||||| ::||| ::||| ::||| ::|||
20 YAlaAlaIleTyrTyrHisIleGluHisGlyGluGluLysIleSerArgA 37
 ||||| ::||| ::||| ::||| ::|||
57 GCGCGGATCTTCGAAGTCTGGAGAGCCACACTGGGAG..... 96
 ||||| ::||| ::||| ::||| ::|||
37 laGluGlnArgLysAlaGlnIleAlaIleAsnGluTyrLeuLeuGluGlu 53
 ||| ::||| ::||| ::||| ::|||
97 ..GAGGCCAAGAAACTACTACACACAGAAAGTGCATCTCTCAAGGAG 144
 ::: ::||| ::||| ::||| ::|||
54 LeuGlyAspLysAsnThrThrThrGlnAspGluIleLeuGlnArgIleSe 70
 ::: ::||| ::||| ::||| ::|||
145 TTCCTCGTCCCTGAGGAGGCGCTGGACAAGATCCTAGAGTGGTATC 194
 ||||| ::||| ::||| ::||| ::|||
70 rAspTyrCysAspLysProValThrLeuProProThrTyrAspAspThrp 87
 ||||| ::||| ::||| ::||| ::|||
195 TCATCTGCAGGACAGGCTGGCCATC.....ACAGGGAACACAGACCT 238
 ||||| ::||| ::||| ::||| ::|||
87 rOTyrThrTrpThrPheTyrHisAlaPhePheAlaPheThrValcys 103
 ::: ::||| ::||| ::||| ::|||
239 TCAACAACCTGGAACCTGCGCCCAATGCAATGATTTTGCAGCAGCCCTCAT 288
 ::: ::||| ::||| ::||| ::|||
104 SerThrValGlyTyrGlyAsnIleSerProThrThrPheAlaGlyArgMe 120.
 ::: ::||| ::||| ::||| ::|||
289 ACCACCATGGATGCAATGTGGCTCCCAAGAGACCCCGCGCTCGCCT 338
 ::: ::||| ::||| ::||| ::|||
120 tIleMetIleAlaTyrSerValIleGlyIleProValAsnGlyIleLeup 137
 ::: ::||| ::||| ::||| ::|||
339 CTTCTGTTTCTATGGTCTCTTCGGGGTCCCGCTGCGCTGACGTGGA 388
 ::: ::||| ::||| ::||| ::|||
137 heAlaGlyLeuGlyGluTyrPheGlyArgThrPheGluAlaIleTyrArg 153
 ::: ::||| ::||| ::||| ::|||
389 TCAGTGCCTGGCAAGTCTCTCGG.....GGA 417
 ::: ::||| ::||| ::||| ::|||
154 ArgTyrLysTyrLysMetSerThrAspMetHisTyrValProG1 170
 ||| ::||| ::||| ::||| ::|||
418 CGTCCCAAGAGACTAGGCGAGTCTCTTACCAAGAGAGGTGTGAGTCTGCG 467
 ::: ::||| ::||| ::||| ::|||
170 nLeuGlyLeuIleThrThrValValIleAlaLeuIleProGlyIleAlaL 187
 ::: ::||| ::||| ::||| ::|||
468 GAAGGCCAGATCAGTGCAGCTCATCTTTCATCGTGGGGCGCTCCTAG 517
 ::: ::||| ::||| ::||| ::|||
187 euPheLeuValProCysValGlyValHisLeuLeuArgGluLeuGly 203
 ::: ::||| ::||| ::||| ::|||
518 TCCACCTGGTATCCCACTTC...GTATTCAATGGTGAAGT...GGG 561
 ::: ::||| ::||| ::||| ::|||
204 LeuSerSerile....SerLeuTyrTyrSerTyrValThrThrThrI1 219
 ::: ::||| ::||| ::||| ::|||
562 TGGAGTACATCAGAGGCGCTTACTACTCTCTCATCACCATCTCCACCAT 611
 ::: ::||| ::||| ::||| ::|||
219 eGlyPheGlyAspTyrValProThrPheGlyAlaAsnGlnProLysGluP 236
 ::: ::||| ::||| ::||| ::|||
612 CGGCTTCGGTGAATTTGGGCC.....GGTGTGAACCCAGC..... 648
 ::: ::||| ::||| ::||| ::|||
236 heGlyGlyTrpPheValTyrGlnIlePheValIleValTrpPheIle 252
 ::: ::||| ::||| ::||| ::|||
649 ..GCCAACTACCAAGCGCTGTACCGCTACTTCTGTGAGCTCTGAGTCTAC 696
 ::: ::||| ::||| ::||| ::|||
253 PheSerLeuGlyTyrLeuValMetIleMetThrPhe..... 264
 ::: ::||| ::||| ::||| ::|||
697 TTGGGCTGGCGTGTCTCCCTTTTGTCAACTGGAAGGTGAGCATGTT 746
 ::: ::||| ::||| ::||| ::|||

```
265 .....IleThrArgGlyLeuGlnSerLysLysLeuAlaTyrLeuGluG 279
    : : : : : : : : : : : : : : : : : : : : : : : :
747 TGTGGAAGTCCCAAGCCATTAAAGCGGGCGCGGCGGCGGAGGAGT 796
    : : : : : : : : : : : : : : : : : : : : : : : :
279 InGlnLeuSerSer.....AsnLeuLysAlaThrGlnAsnArgIleTrp 293
    : : : : : : : : : : : : : : : : : : : : : : : :
797 CCTTTGAGAGCTCCCCACACTCCCGAAGCGCTCGAGGTGAAG...GGG 843
    : : : : : : : : : : : : : : : : : : : : : : : :
294 SerGlyValThrLysAspValGlyTyrLeuArgArgMetLeuAsnGluLe 310
    : : : : : : : : : : : : : : : : : : : : : : : :
844 AGCACAGCTCCCAAGGACGCTCAACATCTTCAGC..... 876
    : : : : : : : : : : : : : : : : : : : : : : : :
310 uTyrIleLeuLysValLysProValTyrThrAspVal.....AspIleA 325
    : : : : : : : : : : : : : : : : : : : : : : : :
877 .TTTCTTCCAAAGAGAGACCTACAAACGACCTCATCAAGCAGATCG 925
    : : : : : : : : : : : : : : : : : : : : : : : :
325 IaTyrThrLeu..... 328
    : : : : : : : : : : : : : : : : : : : : : : : :
926 GGAAGAGCCCATGAAGACAAGCGGGGTGGGAGACGGCGCGGCCCA 975
    : : : : : : : : : : : : : : : : : : : : : : : :
329 .....ProArgSerAsnSerCysProAspLeuSerMetTyrArgVa 342
    : : : : : : : : : : : : : : : : : : : : : : : :
976 GGGCTGGGCGCTCAAGCGCGTGGCTCCAGCACACTGCCCTTCCCTGT 1025
    : : : : : : : : : : : : : : : : : : : : : : : :
342 lGluProAlaProIleProSerArgLysArgAlaPheSerValCysAlaA 359
    : : : : : : : : : : : : : : : : : : : : : : : :
1026 G...CCCTGGTAGTCTACTCCAAAGAACCGGTG...CCACGCTTGAAG 1069
    : : : : : : : : : : : : : : : : : : : : : : : :
359 sPheMetValGlyAlaGlnArgGluAlaGlyMetValHisAlaAsnSer 375
    : : : : : : : : : : : : : : : : : : : : : : : :
1070 AGGTGTACAGACCTGAGGAGCAAGGCGACGATCAAGGTCGCCAGAT 1119
    : : : : : : : : : : : : : : : : : : : : : : : :
376 ThrAspLeuThrLysLeuAspArgGluLysThrPheGluThrAlaGluAl 392
    : : : : : : : : : : : : : : : : : : : : : : : :
1120 GAGGAGGTGTGGCAGCGGCCCTGAAGACAGCTCCCTGTCGCCCGAGT 1169
    : : : : : : : : : : : : : : : : : : : : : : : :
392 aTyrHisGlnThrThrAspLeuLeuAlaLysValValAsnAlaLeuAla 409
    : : : : : : : : : : : : : : : : : : : : : : : :
1170 GTTCATGACACAGCTGGACCGCATCAGCGAG..... 1200
    : : : : : : : : : : : : : : : : : : : : : : : :
409 hrValLysProProAlaGluGlnGluAspAlaAlaLeuTyrGlyGly 425
    : : : : : : : : : : : : : : : : : : : : : : : :
1201 .....GAATGCGAGCATGGGAGCGGCCAGGAC..... 1227
    : : : : : : : : : : : : : : : : : : : : : : : :
426 TyrHisGly.....PheSerAspSerGlnIleLeuAlaSerGluTrpSe 440
    : : : : : : : : : : : : : : : : : : : : : : : :
1228 TACCACCCACTCATCTTCAGGAGCGCCACATCCTTCGTGAACACGGA 1277
    : : : : : : : : : : : : : : : : : : : : : : : :
440 rPheSerThrValAsnGluPheThrSerProArgArgProAlaAlaArg 457
    : : : : : : : : : : : : : : : : : : : : : : : :
1278 GGCTGGCTCTCTCAGACGAGGAGACCTCC.....AAGT 1309
    : : : : : : : : : : : : : : : : : : : : : : : :
457 IaCysSerAspPheAsnLeu.....GluAlaProArgTrp..... 468
    : : : : : : : : : : : : : : : : : : : : : : : :
1310 CCTCGCTAGAGACACACTGGCAGGGAGGAGAGCCCGGAGGGGGCT 1359
    : : : : : : : : : : : : : : : : : : : : : : : :
469 GlnSerGluArgProLeuArg.....SerSerHisAsnGluTrp 481
    : : : : : : : : : : : : : : : : : : : : : : : :
1360 GAAGCCAAAGCGCCCTGAACATGGCGAGTTCCTCTCTCTCCGAGTC 1409
    : : : : : : : : : : : : : : : : : : : : : : : :
481 pThrTrpSerGlyAspAsnGlnGlnIleGlnGluAlaPheAsnGlnArg 498
    : : : : : : : : : : : : : : : : : : : : : : : :
1410 CACCTTCACGACACTGAGTCTGTGAGCTCTGTGCTTACGAACAGCTGA 1459
    : : : : : : : : : : : : : : : : : : : : : : : :
498 yrLysGlyGlnGlnArgAlaAsn 505
    : : : : : : : : : : : : : : : : : : : : : : : :
1460 TGAATGAGTACAAACAGGCTAAC 1482
    : : : : : : : : : : : : : : : : : : : : : : : :
```

seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA1999.DAT:z10607

seq_documentation_block:

ID z10607 standard; cDNA; 1993 BP.

```
XX AC z10607;
XX :
XX DT 18-NOV-1999 (first entry)
XX :
XX DE cDNA encoding a mechanically sensitive potassium channel protein TREK-1.
XX :
XX KW Mechanically sensitive potassium channel protein; TREK-1;
XX KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;
XX KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;
XX KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;
XX KW muscular disease; ds.
XX :
XX OS Mus sp.
XX :
XX FH Key Location/Qualifiers
XX CDS 484..1596
XX :
XX FT /*tag= a
XX :
XX PN WO9945108-A2.
XX :
XX PD 10-SEP-1999.
XX :
XX PF 23-FEB-1999; 99WO-FR00404.
XX :
XX PR 05-MAR-1998; 98FR-0002725.
XX :
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX :
XX PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;
XX :
XX DR WPI; 1999-551038/46.
XX :
XX DP P-PSDB; Y30648.
XX :
XX PT New mechanically sensitive potassium channel, used to screen for
XX PT specific modulators, potential therapeutic agents for heart and nervous
XX PT system disorders
XX :
XX PS Claim 7; Page 23-25; 40pp; French.
XX :
XX CC The present sequence encodes a mechanically sensitive potassium
XX CC channel protein designated TREK-1. The protein is activated by
XX CC polyunsaturated fatty acids, particularly arachidonic acid, and by
XX CC riluzole. The protein is used to screen for specific modulators which
XX CC are useful for treating or preventing diseases of the heart and nervous
XX CC systems in humans and animals, e.g. epilepsy, cardiovascular disease
XX CC (arrhythmia), neurodegeneration (particularly where associated with
XX CC ischemia or anoxia), abnormalities of hormone secretion and muscular
XX CC disease. The protein itself may be used to treat these diseases.
XX CC Antibodies specific for the protein are used to detect it in tissues,
XX CC also as therapeutic inhibitors or activators.
XX :
XX SQ Sequence 1993 BP; 426 A; 570 C; 561 G; 436 T; 0 other;
```

alignment_scores:

Quality:	298.50	Length:	316
Ratio:	1.588	Gaps:	13
Percent Similarity:	59.494	Percent Identity:	28.481

alignment_block:

US-08-816-011c-2 x z10607

Align seg 1/1 to: z10607 from: 1 to: 1993

```
9 LeuLeullePheTyrIleSerTyrLeuMetPheGlyAlaAlaIleTyrTy 25
: : : : : : : : : : : : : : : : : : : : : : : :
631 ATTTTCCTGGTGGTCTGCTCTACCTGATCATCGGAGCGCGGTGTCAA 680
: : : : : : : : : : : : : : : : : : : : : : : :
25 rHisIleGluHisGlyGluGluLysIleSerArgAlaGluGlnArgLysA 42
: : : : : : : : : : : : : : : : : : : : : : : :
681 GGCATTGGAGCAGCCCTCAGGAG.....ATTCCCGAGAGACCA 718
: : : : : : : : : : : : : : : : : : : : : : : :
```

```
42 laGlnIleAlaIleAsnGluTyrLeuLeuGluLeuGlyAspLysAsn 58
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
719 CCATTGTGATCCAGAACGACCTTCATAGCCAGCATGCTCGCTCAAC 768
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
59 ThrThrGlnAspGluLeuGlnArgIleSerAspTyrCysAspLys 75
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
769 TCCACCGAGCTGGAGAACTCATCAGCAATAATAGTGGCAGCAATAAAGC 818
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
75 sProValThrLeuProProThrTyrAspAspThrProTyrThrTrpThr 92
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
819 AGGATATTCCCTTAGGAACAGCTCCATCAAGTTAGTCACTGGGACC 868
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
92 heTyrHisAlaPhePheAlaPheThrValCysSerThrValGlyTyr 108
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
869 TCGGAAGCTCTTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 918
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
109 GlyAsnIleSerProThrThrPheAlaGlyArgMetIleMetIleAla 125
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
919 GGAACATCTCCCAAGCACTGGAAGGTGGAATAATTTCTGCATCATCTA 968
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
125 rSerValIleGlyIleProValAsnGlyIleLeuPheAlaGly..... 139
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
969 TGCCTTGTGGAATCCCTCTTTGCTTCTTCTGCTGCTGCTGCTGCTGCTG 1018
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
140 .....LeuGlyGluTyrPheGlyArgThrPheGluAlaIleTyrArg 154
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1019 ATCAGCTAGGAACATATATTTGGAAGAAGATTTGCCAAGTGGAGACACA 1068
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
155 TyrLysLysTyrLysMetSerThrAspMetHisTyrValProGlnLe 171
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1069 TTTATTAGTGAATGTTAGT.....CAGACGAAGAT 1100
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
171 uGlyLeuIleThrThrValValIleAlaLeuIleProGlyIleAlaLeu 188
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1101 TCGTATCATCTCCACCATCATCTTCTTCTTCTTCTTCTTCTTCTTCTT 1147
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
188 heLeuValLeuProCysValGlyValHisLeuLeuArgGluLeu....Gly 203
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1148 TTGTGGCTCTCCCTCGCGTC.....ATATTCAAGCATATAGAAGC 1188
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
204 LeuSerSerIle...SerLeuTyrTyrSerTyrValThrThrThrIle 219
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1189 TGGAGCCCTCGGAGCGTATCTATTTTGTGGTTATCTACTCTGACGACCAT 1238
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
219 eGlyPheGlyAspTyrValProThrPheGlyAlaAsnGlnProLysGlu 236
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1239 TGGATTGGAGACTACGTGGCA.....1260
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
236 heGlyGlyTrpPheValValTyrGlnIlePheVal.....IleValTrp 250
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1261 ..GGTGGATCAGACATTGAATATCTGGACTCTTACAAGCCTGTGTGTGG 1308
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
251 Phe.....IlePheSerLeuGlyTyrLeuValMetIleMetThrPheIle 265
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1309 TTCTGGATCTCTGTGGCTGGCCCTACTTTGACGCTGTTCTGACCATGAT 1358
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
265 eThrArgGlyLeuGln.....SerLysLysLeuAlaTyrLeuGluGln 280
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1359 TGGGACTGGCTACGGGTGATCTCTAAGAAG.....ACGAAGG 1396
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
280 InLeuSerSerAsnLeuLysAlaThrGlnAsnArgIleTrpSerGlyVal 296
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1397 AAGAGGTGGAGAGTTTCAGAGCGCATCCCGCTGAGTGGAGCAATGTC 1446
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
297 ThrLysAspValGlyTyrLeuArgArgMetLeuAsn...GluLeuTyr 311
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1447 ACGCCGAGTTCAAGGAACAGGAGCGGCTGAGCGTGGAGATCTAC 1494
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
```

```
seq_name: /cqn2_2/gcgdata/geneseq/geneseq/NA1999.DAT:200040
seq_documentation_block:
ID 200040 standard; DNA; 1994 BP.
XX
```

```
AC 200040;
XX 12-OCT-1999 (first entry)
XX Mouse h-TREK1 polynucleotide.
XX h-TREK1; two pore potassium channel; inflammatory disease;
KW chromosome 1q32; ss.
XX Mus musculus.
XX Key Location/Qualifiers
FT CDS 484..1719
FT /*tag= a
FT /product= "h-TREK1"
XX
XX WO937762-A1.
XX 29-JUL-1999.
XX 02-DEC-1998; 98WO-EF07805.
XX 09-OCT-1998; 98GB-0022135.
XX 27-JAN-1998; 98EP-0300570.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX Chapman CG, Meadows HJ;
XX WPI; 1999-469126/39.
XX P-PSDB; Y28497.
XX New two pore potassium channel used for, e.g. treatment of cancer,
XX pulmonary, cardiovascular and inflammatory diseases
XX Claim 9; Page 25-26; 44pp; English.
XX This sequence is the h-TREK1 polynucleotide from the mouse, encoding the
XX h-TREK1 polypeptide Y28496. h-TREK1 is a two pore potassium channel.
XX The polynucleotide sequence of h-TREK1 can be used to diagnose a disease
XX or susceptibility to a disease related to expression or activity of
XX h-TREK1 polypeptides. The methods of diagnosis may be used in the
XX treatment of diseases including cancer, pulmonary, cardiovascular, and
XX inflammatory diseases, pain, psychiatric disorders including depression
XX and schizophrenia, neurodegenerative diseases including Alzheimer's,
XX stroke, and head trauma and neurological disorders including migraine.
XX Sequence 1994 BP; 426 A; 561 C; 561 G; 446 T; 0 other;

alignment_scores:
Quality: 298.50 Length: 316
Ratio: 1.588 Gaps: 13
Percent Similarity: 59.494 Percent Identity: 28.481

alignment_block:
US-08-816-011c-2 x Z00040 ..
Align seg 1/1 to: Z00040 from: 1 to: 1994

9 LeuLeuIlePheTyrIleSerTyrLeuMetPheGlyAlaIleTyrTy 25
:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
631 ATTTTCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 680
:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
25 rHisIleGluHisGlyGluGluLysIleSerArgAlaGluGluArgLys 42
:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
681 GGCATTGGAGCAGCTCAGGAG.....ATTCCCAGAGGACCA 718
:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
42 laGlnIleAlaIleAsnGluTyrLeuLeuGluLeuGlyAspLysAsn 58
:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
719 CCATTGTGATCCAGAACGACCATCTCATAGCCAGCATGCTCGCTCAAC 768
:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
59 ThrThrThrGlnAspGluIleLeuGlnArgIleSerAspTyrCysAspLys 75
```

75 s p r o v a l t h r L e u P r o P r o t h r T y r A s p A s p T h r P r o T y r T h r T r o T h r p 92

XX
DE
K-TPK1 0019860100

CC it is likely that abnormal potassium channels are also implicated in
 CC certain renal, cardiovascular and central nervous system (CNS) disorders.
 CC Nucleotides encoding K+nov proteins may be used for identifying
 CC homologous or related proteins and the DNA sequences encoding them. They
 CC may be used to produce compositions that modulate the expression and
 CC function of the K+nov protein and in studying the biochemical pathways
 CC associated with it. They may also be used for the recombinant production
 CC of K+nov protein in fermentation cultures. Additionally, such
 CC nucleotides may be used in gene therapy protocols for the treatment
 CC of diseases associated with abnormal potassium channels.
 xx

5Q Sequence 3300 BP; 997 A; 629 C; 680 G; 994 T; 0 other;

alignment_scores:

Quality: 292.50 Length: 428
 Ratio: 1.306 Gaps: 18
 Percent Similarity: 52.336 Percent Identity: 25.234

alignment_block:

US-08-816-011c-2 x z11915 ..

Align seg 1/1 to: z11915 from: 1 to: 3300

9 LeuLeuIlePheTyrIleSerTyrLeuMetPheGlyAlaAlaIleTyrTy 25
 197 ATATTCCTGGTGGTTCCTCTATCTATCTGATCGGAGCCACCGTGTCAA 246
 25 rHisIleGluHisGlyGluGluLysIleSerArgAlaGluGlnArgLysA 42
 247 AGCATTTGGAGAGCCTCATGAG.....ATTTCACAGAGGACCA 284
 42 laeGlnIleAlaIleAsnGluTyrLeuGluGluLeuGlyAspLysAsn 58
 285 CCATTCTGTGATCCAGAACCAACATTCATATCCCAACATTCCTGTGCAAT 334
 59 ThrThrThrGlnAspGluIleLeuGlnArgIleSerAspTyrCysAsp 75
 335 TCGACGAGCTGGATGAACATTCACGAAATAGTGGCAGCAATAATGC 384
 75 sProValThrLeuProProThrTyrAspThrProTyrThrTrpThrP 92
 385 AGGATATACCGTTAGGAACACCTCCCAATCAATCAGTCACTGGGATT 434
 92 heTyrHisAlaPhePheAlaPheThrValCysSerThrValGlyTyr 108
 435 TGGGAAGTTCCCTTCTTCTTGGTGGCAGCTGTTATTACACCATAGGATT 484
 109 GlyAsnIleSerProThrThrPheAlaGlyArgMetIleMetIleAla 125
 485 GGAACATCTCACCGCAGCAGCAAGCGGCAAAATATTCTGTATCATCTA 534
 125 rSerValIleGlyIleProValAsnGlyIleLeuPheAlaGly..... 139
 535 TGCCTTACTGGGAATTCCTCTTGGTTCCTTCTTGGTGGAGTTGGAG 584
 140LeuGlyGluTyrPheGlyArgThrPheGluAlaIleTyrArg 154
 585 ATCAGCTAGGCACCATATTGGAAAAGGAATTCGCCAAGTGGGAAGATACG 634
 155 TyrLysLysTyrLysMetSerThrAspMetHisTyrValProGlnLe 171
 635 TTTATTAAGTGAATTTAGT.....CAGACCAAGAT 666
 171 uGlyLeuIleThrThrValValIleAlaLeuIleProGlyIleAlaLeu 188
 667 TCGCATCATCTCAACATCATATTTATATATT...GGCTGTGTACTCT 713
 188 heLeuValLeuProCysValGlyValHisLeuLeuArgGluLeu...Gly 203
 714 TTGTGGCTCTGGCTGGATC.....ATATTCAACACATAGAGGC 754
 204 LeuSerSerIle...SerLeuTyrTyrSerTyrValThrThrThrI 219

755 TGGAGTGCCCTGGACCCCTATTATTGTTGGTTATCACTCTAACAACTAT 804
 219 eGlyPheGlyAspTyrValProThrPheGlyAlaAsnGlnProLysGluP 236
 805 TGGATTGGTGACTAGCTTGA..... 826
 236 heGlyGlyTrpPheValValTyrGlnIlePheVal.....IleValTrp 250
 827 ..GGTGGATCCGATATTGAATATCTGGACTTCTATAAGGCTGTCGTGG 874
 251 Phe.....IlePheSerLeuGlyTyrLeuValMetIleMetThrPheI 265
 875 TTCTGGATCCTTGTAGGGCTTGTCTTACTTTGCTGCTGCTGAGCATGAT 924
 265 eThrArgGlyLeuGln.....SerLysLysLeuAlaTyrLeuGluGln 280
 925 TGGAGATTGGCTCCGAGTATATAAAG.....ACAAAG 962
 280 InLeuSerSerAsnLeuLysAlaThrGlnAsnArgIleTrpSerGlyVal 296
 963 AAGAGCTGGGAGAGTTTCAGAGCACACGCTCTGAGTGGACAGCAACGTC 1012
 297 ThrLysAspValGlyTyrLeuArgArgMetLeuAsnGluLeuTyrIle 313
 1013 ACAGCGAATTCAAAGAAACAGGAGCGGAGT..... 1048
 313 uLysValLysProValTyrThrAspValAspIleAlaTyrThrLeuPro 330
 1049GTGAGATTATGACAACTGCTCCAGC 1073
 330 rGSerAsnSerCysProAspLeuSerMetTyrArgValGluProAlaPro 346
 1074 GGGCCACCTCCATC..... 1087
 347 IleProSerArgLysArgAlaPheSerValCysAlaAspMetValGlyAl 363
 1088AAGCGGAAGCTCTCG.....GCAGAACTGGCTGGA.. 1117
 363 aGlnArgGluAlaGlyMetValHisAlaAsnSerAspThrAspLeuThr 380
 1118AACCAATCAGGAGCTGACTC 1139
 380 ysLeuAspArgGluLysThrPheGluThrAlaGluAlaTyrHisGlnThr 396
 1140 CTGTAGGAGG.....ACCTGTCTGAGTGAACCACTGACC 1174
 397 ThrAspLeuLeuAlaLysValValAsnAlaLeuAlaThrValLysPro 413
 1175 AGCGAG.....AGGATGCTCTTGCCTCC 1197
 413 oProAlaGluGlnGluAspAlaAlaLeuTyrGly 424
 1198 CTACTGAGAGCTGAGAGTATCTATCTGAATGTT 1231

seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA2000.DAT:A27105

seq_documentation_block:

ID: A27105 standard; CDNA; 1182 BP.

XX A27105;

XX 04-AUG-2000 (first entry)

XX Human h-TRAAK cDNA sequence #1.

XX Human; h-TRAAK; potassium channel polypeptide;

KW 2P domain potassium channel; neurodegenerative disease; stroke;

KW psychiatric disorder; neurological disorder; Gene therapy; ss.

XX Homo sapiens.

XX OS

XX FH

XX Key

XX Location/Qualifiers

```

FT CDS 1..1182
FT FT /*tag= a
XX /product= h-TRAAK protein #1
XX WO200026253-A1.
XX PD 11-MAY-2000.
XX XX
XX PF 03-NOV-1999; 99WO-GB03634.
XX XX
XX PR 03-NOV-1998; 98GB-0024048.
XX PR 07-OCT-1999; 99GB-0023668.
XX XX
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX XX
XX PI Chapman CG, Duckworth DM;
XX DR WPI; 2000-365583/31.
XX DR P-PSDB; Y94425.
XX
XX Novel isolated h-TRAAK polypeptides belonging to the potassium channel
XX PT family of polypeptides, useful for the diagnosis and treatment of
XX PT h-TRAAK related disorders, e.g. depression and schizophrenia
XX PS
XX PS Claim 5; Page 21; 35pp; English.
XX
XX Functional genomics was used to identify h-TRAAK polypeptides and
XX CC h-TRAAK polynucleotides from human tissue samples. h-TRAAK
XX CC polypeptides have homology to the 2p domain potassium channel family of
XX CC polypeptides. The h-TRAAK polypeptides and polynucleotides may
XX CC be used in diagnostic assays for conditions related to h-TRAAK
XX CC imbalance and for identifying agonists and antagonists of h-TRAAK
XX CC polypeptides. The h-TRAAK polypeptides and polynucleotides may also
XX CC be useful for treatment and prevention (e.g. as vaccines) of certain
XX CC diseases, such as pain, psychiatric disorders including depression and
XX CC schizophrenia, neurodegenerative diseases including Alzheimer's, stroke
XX CC and head trauma and neurological disorders including migraine and
XX CC epilepsy. The present sequence is human h-TRAAK-1 cDNA sequence #1.
XX
XX SQ Sequence 1182 BP; 180 A; 408 C; 377 G; 217 T; 0 other;

alignment_scores:
Quality: 286.00 Length: 319
Ratio: 1.634 Gaps: 11
Percent Similarity: 54.859 Percent Identity: 27.900

alignment_block:
US-08-816-011c-2 x A27105 ..
Align seg 1/1 to: A27105 from: 1 to: 1182
7 IleLeuLeuLeuIlePheTyrIleSerTyrLeuMetPheGlyAlaAlaI 23
::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
19 CTGGCCCTGTGGCGGTGGTCTTCTTACTTGTGTGGTGGTGGTGGT 68
::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
23 eTyrTyrHisIleGluHisGlyGluGluLysIleSerArgAlaGluGlnA 40
::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
69 GTTCCGGGCGCTGGAGCAGCCCCACGAG.....C 97
::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
40 rgLysAlaGlnIleAlaIleAsnGluTyrLeuLeuGluLeuGlyAsp 56
::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
98 AGCAGGCCAGAGGAGGCTGGGGAGGTCCGAGAGAAGTTCCTGAGGGCC 147
::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
57 LysAsnThrThrGlnAspGluIleuGlnArgIleSerAspTyrCy 73
::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
148 CATCCGTGTGTGACCGACGAGGAGCTGGCTCTCATCAAGGAGGTGGC 197
::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
73 sASP.....LysProValThrLeuProProThrTyrA 84
::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
198 TGATGCCCTGGAGGGGTGGGACCCAGAAACC....AACTCGACCAAGCA 244
::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
84 sASPThrProTyrThrTrpThrPheTyrHisAlaPhePheAlaPhe 100
::: ||||| ::::: ||||| ::::: ||||| ::::: |||||

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seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA2000.DAT:A27106

seq_documentation_block:

ID A27106 standard; cDNA: 1218 BP.

XX

AC A27106;

XX

DT 04-AUG-2000 (first entry)

XX

DE Human h-TRAAK cDNA sequence #2.

XX

KW Human; h-TRAAK; potassium channel polypeptide;

KW 2p domain potassium channel; neurodegenerative disease; stroke;

KW psychiatric disorder; neurological disorder; Gene therapy; ss.


```

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 37..1218
XX FT /*tag= a
XX FT /product= h-TRAAK protein #2
XX PN WO200026253-A1.
XX PD 11-MAY-2000.
XX PF 03-NOV-1999; 99WO-GB03634.
XX PR 03-NOV-1998; 98GB-0024048.
XX PR 07-OCT-1999; 99GB-0023668.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Chapman CG, Duckworth DM;
XX DR WPI; 2000-365583/31.
XX DR P-PSDB; Y94426.
XX PT Novel isolated h-TRAAK polypeptides belonging to the potassium channel
XX PT family of polypeptides, useful for the diagnosis and treatment of
XX PT h-TRAAK related disorders,e.g. depression and schizophrenia -
XX PS Claim 11; Pages 21 and 22; 35pp; English.
XX CC Functional genomics was used to identify h-TRAAK polypeptides and
XX CC h-TRAAK polynucleotides from human tissue samples. h-TRAAK
XX CC polypeptides have homology to the 2P domain potassium channel family of
XX CC polypeptides. The h-TRAAK polypeptides and polynucleotides may
XX CC be used in diagnostic assays for conditions related to h-TRAAK.
XX CC imbalance and for identifying agonists and antagonists of h-TRAAK.
XX CC polypeptides. The h-TRAAK polypeptides and polynucleotides may also
XX CC be useful for treatment and prevention (e.g. as vaccines) of certain
XX CC diseases, such as pain, psychiatric disorders including depression and
XX CC schizophrenia, neurodegenerative disease including Alzheimer's, stroke
XX CC and head trauma and neurological disorders including migraine and
XX CC epilepsy. The present sequence is human h-TRAAK cDNA sequence #2.
XX SQ Sequence 1218 BP; 182 A; 421 C; 395 G; 220 T; 0 other;

alignment_scores:
    Quality: 286.00      Length: 319
    Ratio: 1.634         Gaps: 11
    Percent Similarity: 54.859      Percent Identity: 27.900

alignment_block:
US-08-816-011c-2 x A27106 ..
Align seg 1/1 to: A27106 from: 1 to: 1218
7 IleLeuLeuLeuPheTyrIleSerTyrLeuMetPheGlyAlaAla1 23
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
55 CTGGCCCTGCTGGCGTGTCTTGTCTTACTTGGTGTCTGCTGGT 104
23 eTyrTyrHisIleGluHisGlyCluCluLysIleSerArgAlaGlu1na 40
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
105 GTTCGGGGCCCTGGAGCAGCCCCACGAG.....C 133
40 rGlyAlaGlnIleAlaIleAsnGluTyrLeuLeuGluGluLeuGlyAsp 56
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
134 AGCAGCCCGAGGGAGCTGGGGAGGTCGAGAGAGTTCCTGAGGGCC 183
57 LysAsnThrThrThrGlnAspGluIleLeuGlnArgIleSerAspTyrCy 73
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
184 CATCGGTGTGTGAGCAGCAGGAGGTGGCCCTCTCATCAGGAGGTGGC 233
73 sasp.....LysProValThrLeuProProThrTyrA 84

```

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::||| ||| ||| |||
234 TGATGCCCTGGAGGGGTGGGACCCAGAAACC...AACTCGACCAGCA 280
84 spAspThrProTyrThrThrPheTyrHisAlaPhePheAlaPhe 100
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
281 ACAGCAGCCACTCAGCCTGGGACCTGGGCGCCCTCTTTTCTCAGGG 330
101 ThrValCysSerThrValGlyTyrGlyAsnIleSerProThrThrPheAl 117
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
331 ACCATCATCACCACCATCGCTATGCAATGTGGCCCTGCACAGATGC 380
117 aGlyArgMetIleMetIleAlaTyrSerValIleGlyIleProValAsnG 134
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
381 CGGGCGCCTCTTCTGCATCTTTATCGCTGGTGGGGATTCCGCTGTTCG 430
134 lyIleLeuPheAlaGlyLeuGlyGluTyrPheGlyArgThr..... 147
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
431 GGATCCTACTGGCAGGGTGGGGACCGCTGGCTCCTCCCTGCCCAT 480
148 .....PheGluAlaIleTyrArgArgTyrLysLysTyrLysMe 160
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
481 GGCATCGGTACATTTGAAGCATCTTCTTGAAGTGG..... 516
160 tSerThrAspMetHisTyrValProGlnLeuGlyLeuIleThrThrV 177
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
517 .....CAGTGGCCACCGGAGCTAGTAAGAGTGTCTCGG 550
177 alValIleAlaLeuIleProGlyIleAlaLeuPheLeuValLeuProCys 193
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
551 CGATGCTTTCCTGCTGATCGCTGCTCTTTGTCTCAGCCGCCACG 600
194 ValGlyValHisLeuLeuArgGluLeuGlyLeuSerSerIleSerLeuTy 210
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
601 TTC...GTCTTCTGTATATGGAGGACTGGAGCAAGCTGGAGGCCATCTA 647
210 rTyrSerTyrValThrThrThrThrIleGlyPheGlyAspTyrValProT 227
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
648 CTTTGTGTAGTACGCTTACCACCGTGGCTTGGCGACTATGTGGCC. 696
227 hrPheGlyAlaAsnGlnProLysGluPheGlyGlyTrpPheValValTy 243
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
697 .....GGCGGGACCCAGCAGGAC.....TCCCGGCTAT 729
244 GlnIlePheValIleValTrpPheIlePheSerLeuGlyTyrLeuValMe 260
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
730 CAGCCGCTGGTGTGTCTGTGATCTGCTCGGCTGGCTTACTTCTGCTC 779
260 tIleMetThrPheIleThrArgGlyLeuGln.....S 271
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
780 AGTGCTCACCACTCGGAAGTGGCTGGAGTAGTGTCCCGCCGCACTC 829
271 erLysLysLeuAlaTyrLeuGluGlnGlnLeuSerSerAsnLeuLysAla 287
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
830 GGCAGAGATGGCGCCCTCAGGCTCAGGCTGCCAGC..... 867
288 ThrGlnAsnArgIleTrpSerGly.....ValThrLysAs 299
::: ||||| :::: ||||| :::: ||||| :::: ||||| ::
868 .....TGGACTGGCAGAGTGACAGCGCGGTGACCCAGCG 902
299 pValGly 301
903 AGCCGGG 909
seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA2000.DAT:298176
seq_documentation_block:
XX Z98176 standard; cDNA; 1551 BP.
XX Z98176;
XX 11-MAY-2000 (first entry)
XX Human signal peptide containing protein HSPp-68 cDNA SEQ ID NO:202.

```



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748 ..... 748
293 TtpSerGlyValThrLysAspValGlyTyrLeuArgArgMetLeuAsnG1 309
749 .....AA 750
309 uLeuTyrIleLeuLysValLys.ProValTyrThrAspValAspIleAla 325
751 CCTCGTGGTGTCTGCTTCATGACCA..... 776
326 TyrThrLeuProArgSerAsnSerCysProAspLeuSerMetTyrArgVa 342
777 ...TGAAACCGGAGGACGAGACGGC..... 800
342 lGluProAlaProIleProSerArgLysArgAlaPheSerValCysAlaA 359
801 .....ACGCGGAGCACCAGCGC.....TGCTCAC 825
359 spMetValGlyAlaGlnArgGluAlaGlyMetValHisAlaAsnSerAsp 375
826 GCGCAACGGGAGCGGGCGGCGGAGGGGTGGCAGCG..... 866
376 ThrAspLeuThrLysLeuAspArgGluLysThrPheGluThrAlaGluAl 392
867 .....CGCACACTACGGACA..... 881
392 aTyrHisGlnThrThrAspLeuLeuAlaLysValValAsnAlaLeuAla 409
881 ..... 881
409 hrValLysProProAlaGluGlnGluAspAlaAlaLeuTyrGlyGly 425
882 .....CCGCTCATCCACGGCGGAGCGGGCGGGCT..... 917
426 TyrHisGlyPheSerAspSerGlnIleLeuAlaSerGluTrpSerPheSe 442
917 ..... 917
442 rThrValAsnGluPheThrSerProArgArg.....ProA 454
918 .....TCGCAACGCTCTACGGGAGGTGCTGCACCTTCAGTCCAT 957
454 rGlaAlaArgAlaCysSer.....AspPheAsnLeuGluAla 465
958 GTGCTCGTGCCTGTGTGAAGAGCGCGAGAGCTGCAGTACTCCATCC 1007
466 Pro.....ArgTrpGlnSerGluArgProLeuArgSerSerHisAs 479
1008 CCATGATCATCCCGGGGACCTCTCCACGTCGACACGTCGCG..... 1049
479 nGluTrpThrTrpSerGlyAspAsnGlnGlnIleGlnGluAlaPheAsnG 496
1050 .....TGAGC..... 1055
496 lArgTyrLysGlyGlnGlnArgAlaAsnGlyAlaAlaAsnSerThrMet 512
1056 .....AGAGCCACTCGTCGCGGGAGGGCGGCGCTACAGCG... 1094
513 valHisLeuGluProAspAlaLeuGluGlnLeuArgAsnAsnHisar 529
1095 .....ACAGCGCCTCGGACGC..... 1111
529 gValProValAlaSerArgSerPro.....CysArgMetV 542
1112 TGCTGTGAGCGGGGCGGACCGCTCCGCATCAGCTCGGTGTCCACGGG 1161
542 alCysAspValCysPheProSerArgArgSerThrProArgIleIletrp 558
1162 TCTGCACGCCTGTCCACCTTCGCGGCGCTCATGAAGCGCA..... 1202
559 SerAlaSerCysProTrpSerArgTyrProArgValSer.SerArgArgL 575
..... 575
```

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1203 GGAGCTCCGTGTGACTGCCCGGAGGACCTGGGAGACCTGGGGCGCGGG 1252
575 ysProAspProArgTTrpThrThrSerThrArgSerArgArgProPro 591
1253 CGGGGAGACCCCTGCTGG.....GAGCCAGGAGACTGCC 1287
592 ValAsnProIleCysAlaThrAspAlaValArgHisArgProSer 606
1288 CTGCTGCTGCTGCGGAGTGGGACCGCCGACAAACAT...CCCTCA 1329
seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA1997.DAT:T64960
seq_documentation_block:
ID T64960 standard; cDNA; 1894 BP.
XX
AC T64960;
XX
DT 18-MAR-1998 (first entry)
XX
DE TWIK-1 potassium channel cDNA.
XX
KW TWIK-1 potassium channel; screening; diagnosis; transgenic animal;
KW Tandem Of P domains in a Weak Inward rectifying K+; antibody; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 183..1193
FT /tag= a
FT /product= TWIK-1_potassium_channel_protein
XX
PN FR2744730-Al.
XX
PD 14-AUG-1997.
XX
PF 08-FEB-1996; 96FR-0001565.
XX
PR 08-FEB-1996; 96FR-0001565.
XX
(CNRS ) CNRS CENT NAT RECH SCI.
XX
PI Barhanin J, Duprat F, Fink M, Guillemare E, Lazdunski M;
PI Lesage F, Romey G;
XX
DR WPI; 1997-427773/40.
DR P-PSDB; W23397.
XX
PT Nucleic acid encoding new potassium channel designated TWIK-1 -
PT useful for treating channel deficiency diseases, screening for
PT active agents and for diagnosis
XX
PS Claim 3; Figure 1b; 37pp; French.
XX
CC The present cDNA sequence encodes a protein comprising a potassium
CC channel with the properties of a TWIK (Tandem of P domains in
CC a Weak Inward rectifying K+)-1 channel. This is the first member of a new
CC family of channels consisting of 4 transmembrane segments and two P
CC domains, and being only weakly rectifying. The cDNA, vectors, the cells
CC expressing TWIK-1 type channels and the protein are used to compensate
CC for deficiency of potassium channels in various tissues. Compounds
CC for modulating activity of TWIK-1 type channels may also be useful
CC therapeutically, e.g. for control of epilepsy, arrhythmia, vascular
CC disease, neurodegeneration (particularly of ischaemic or anoxic origin),
CC endocrine or muscular disorders. The cDNA and the vectors can also be
CC used to create transgenic animals (especially knock-out animals) for use
CC as models of TWIK-1 related diseases. Analysis of the sequence of the
CC TWIK-1 gene may be used for pre-natal diagnosis of disease. Antibodies
CC can be used to detect TWIK-1 channels and for inhibiting or activating
CC the channels in vivo.
XX
SQ Sequence 1894 BP; 461 A; 435 C; 512 G; 486 T; 0 other;
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alignment_scores:

Quality: 239.00 Length: 263
Ratio: 1.583 Gaps: 8
Percent Similarity: 57.414 Percent Identity: 28.137

alignment_block:

US-08-816-011C-2 x T64960 ..

Align seg 1/1 to: T64960 from: 1 to: 1894

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9 LeuLeuIlePheTyrIleSerTyrLeuMetPheGlyAlaAlaIleTyrTy 25
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
258 CTGGTGGCTGGCTACTCTCTACTGTGCTTCGGCGAGTGGTCTTC 307
25 rHisIleGluHisGlyGluGluLysIleSerArgAlaGluGlnArgLysA 42
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
308 CTCGGTGGAGCTGCCCTATGAGGACCTCTCGCGCAGGAGCTGGCAGAG 356
42 laGlnIleAlaIleAsnGluTyrLeuLeuGluGluLeuGlyAspLysAsn 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
357 .....CTGAAGCGAGCGTCTCTGGAGGAGCAGCAGTGCCTGTCT 395
59 ThrThrThrGlnAspGluIleLeuGlnArgIleSerAspTyrCysAspLy 75
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
396 GAGCAGCAGCTGGGAGCAGTCTCTGGCGCGGTCTGGAGGCCAGCACTA 445
75 sProValThrLeuProThrThrTyrAspThrProThrThrThrP 92
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
446 CGCGGTGTCGTGCTCAGCAGCGCTCGGGCAAC...TGGACTGGGACT 492
92 heTyrHisAlaPhePhePheAlaPheThrValCysSerThrValGlyTyr 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
493 TCAGCTCGCGCTCTCTCTCCAGCAGCAGTGTCTCCACACAGGTTAT 542
109 GlyAsnIleSerProThrThrPheAlaGlyArgMetIleMetIleAlaTy 125
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
543 GCCACACCGTGCCTGTAGATGGAGGTAAAGCGCTTCGCATCATCTA 592
125 rSerValIleGlyIleProValAsnGlyIleLeuPheAlaGlyLeuGlyG 142
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
593 CTCGGTCAATTGGCATTCCTTACC...CTCCTGTTC..... 626
142 LuTyrPheGlyArgThrPheGluAlaIleTyrArgTyrLysLysTyr 158
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
627 .....CTGACGGCTGTGTCTCCAGCGCATCACCGTGCAC 659
159 LysMetSerThrAspMetHisTyrValProProGlnLeuGlyLeu..... 173
660 GTCACCGCGCAGCGCGGCTCTCTACTTCCACATCCGCTGGGCTTCTCCAA 709
174 ....IleThrThrValIleAlaLeuIleProGly.....IleA 186
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
710 GCAGGTGGTGGCCATCGTCCATGCGGTGCTCTGGTGTCTCACTGTGT 759
186 laLeuPheLeuValLeuProCysValGlyValHisLeuLeuArgGluLeu 202
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
760 CCTGCTCTCTTCTTATCCGCGCGCTCTCTCTCAGTCTGGAGGATGAC 809
203 GlyLeuSerSerIleSerLeuTyrTyrSerTyrValThrThrThrII 219
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
810 TGGAACTTCTCGGAATCTTTATTTTGTGTTTATTTTCCCTGAGCACCAT 859
219 eGlyPheGlyAspTyrValProThrPheGlyAlaAsnGlnProLysGluP 236
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
860 TGGCTGGGGATATGCTGCTGGGAGGCTACATCAATAA..... 902
236 heGlyGlyTyrPheValValTyrGlnIlePheValIleValTyrPheIle 252
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
903 .....TTCAGAGAGCTCTAATGATGGATCAGCTGTACCTGCTA 944
253 PheSerLeu...GlyTyrLeuValMetIleMetThrPhe 264
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945 CTTCGCCCTTATGCCATGTGGTAGTCTCGAAACCTTC 983
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seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:X78383

seq_documentation_block:

ID X78383 standard; cDNA to mRNA; 2180 BP.

XX X78383;

XX 25-AUG-1999 (first entry) }

XX Human hTREK-1 cDNA.

XX hTREK-2; Twik-1 Related K+ channel-2; vasotropic; antiinflammatory;
analgesic; treatment; gene therapy; inhibitor; detection; diagnosis;
KW disease susceptibility; cerebral; cardiac; renal; ischemia; brain;
KW inflammation; pain; mimic; neurotransmitter; hormone; chromosome mapping;
KW linkage analysis; mutation; immunogen; human; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 74..1015

XX FT /*tag= a

XX FT /product= "hTREK-2"

XX EP930364-A1.

XX 21-JUL-1999.

XX 16-JAN-1998; 98EP-0400072.

XX 16-JAN-1998; 98EP-0400072.

XX (SYNO) SYNTHELABO.

XX Partiseti M;

XX WPI; 1999-387707/33.

XX P-PSDB; Y25116.

XX New human polypeptides useful for diagnosing and treating cerebral
and cardiac ischemias

XX Claim 5; Page 15-18; 21pp; English.

XX This invention describes a novel human Twik-1 Related K+ channel-2
(hTREK-2) polypeptide (I) and its encoding nucleic acid (II) which has
vasotropic, antiinflammatory and analgesic activity. (II) or agonists of
(I) may be used to stimulate production of (I) in vivo to treat patients
requiring enhanced activity or expression of (I). This use of (II)
represents a gene therapy regime. Antagonists of (I), the complement of
(II) used as an antisense construct or a polypeptide competitor of (I)
may be administered to patients to inhibit activity or expression of (I).
Detection of the presence or amount of (I) in a sample from a patient or
detection of mutations in (I) may be used to diagnose or measure
susceptibility to diseases related to altered expression or activity of
(I). The diseases and conditions resulting from altered activity or
expression of (I) which may be treated as above include cerebral,
cardiac and renal ischemias, brain and cardiac diseases, inflammation
and pain. In addition, (I), (II), and agonists and antagonists of (I)
may be used to mimic or antagonize the effects of endogenous
neurotransmitters and hormones. (II) or its fragments may be used as
hybridization probes to isolate full length and genomic cDNAs encoding
(I) or its homologues from cDNA or genomic libraries. (II) may also be
used for chromosome mapping and linkage analysis to identify the
relationship between genes and diseases which have been mapped to the
same chromosome. In addition (II) may be used to identify mutations
associated with diseases by comparing the sequence of (II) between
affected and unaffected individuals. (I) or its fragments may be used as
immunogens to produce antibodies against (I). Antibodies to (I) may be
used to isolate or identify clones expressing (I) or to purify (I) by
affinity chromatography. These antibodies may also be used to treat the
above diseases as agonists or antagonists of (I).

```
XX
SQ   Sequence 2180 BP; 374 A; 669 C; 645 G; 492 T; 0 other;

alignment_scores:
  Quality: 210.50      Length: 286
  Ratio: 1.442         Gaps: 9
  Percent Similarity: 51.049  Percent Identity: 24.476

alignment_block:
US-08-816-011c-2 x X78383 ..
Align seg 1/1 to: X78383 from: 1 to: 2180

10  LeuIlePheTyrTrpPheGlyLeuMetPheGlyAlaAlaIleTyrTyrHI 26
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104 TTGGCGCGGTACCGCGTACCGCGTACCGCGTACCGCGTACCGCGTACCGCG 153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
26  sIleGluHisGlyGluGluLysIleSerArgAlaGluGlnArgLysAlaG 43
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
154 GCTGGAGGGCGCCACGACCGAGGCTCCGAGCCGAG..... 190
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
43  InIleAlaIleAsnGluTyrLeuGluGluLeuGlyAspLysAsnThr 59
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
191 .....CTGAG..... 196
60  ThrThrGlnAspGluLeuGlnArgIleSerAspTyrCysAspLysPr 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
197 ACCTGCGGGCGGAGCTGCTTACGCG.....AGCCG 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
76  oValThrLeuProThrTyrAsp..... 84
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229 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 278
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279 CCGGACGGCTGGGGGCTGCTTGTCTAACGCTTCGGGGTCCGCCAAC 328
85  AspThrProTyrThrTrpThrPheTyrHisAlaPhePheAlaPheTh 101
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329 GCCTCGGACCCCGCTGGGACTTGGCTCTGCTCTCTCTCTCTCTCTCTCTCT 378
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135 lLeLeuPheAlaGlyLeuGlyGluTyrPheGlyArgThrPheGluAlaI 151
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479 CTGCTGCTGACCGCTCAGCCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 528
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180 AlaLeuIleProGlyIleAlaLeuPheLeuValLeuProCysValGlyIva 196
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seq_documentation_block:

ID Z11914 standard; cDNA; 2571 BP.

XX Z11914;

AC Z11914;

XX Z11914;

DT 30-NOV-1999 (first entry)

XX Human potassium channel K+Hnov49 cDNA.

XX Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;

KW cardiovascular disorder; CNS disorder; renal disorder; ds.

XX Homo sapiens.

XX Key

FT CDS

FT Location/Qualifiers

FT 110..1285

FT /*tag= a

FT /product= "Human K+Hnov49 potassium channel"

FT /note= "No stop codon given in specification"

FT variation

FT 2186

FT /*tag= b

FT /rpt_unit= ATCT

FT /note= "Start site for repeats in 3' untranslated region"

XX W09943696-A1.

XX 02-SEP-1999.

XX 22-FEB-1999; 99WO-US03826.

XX 19-JAN-1999; 99US-0116448.

XX 25-FEB-1998; 98US-0076687.

XX 07-AUG-1998; 98US-0095836.

XX (AXYS-) AXYS PHARM INC.

XX Curran ME, Hu P, Miller AP, Rutter M, Wang J;

XX WPI: 1999-527591/44.

XX P-PSDB; Y34132.

XX New nucleic acids encoding mammalian K+Hnov potassium channel

XX proteins, useful for the diagnosis and treatment of episodic ataxia

XX with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome

XX Claim 4; Page 99-101; 112pp; English.

XX This sequence represents human potassium channel K+Hnov49 cDNA.

XX K+Hnov proteins have a high degree of homology to known potassium

XX channels and may be alpha subunits, which form the functional channel, or

XX accessory subunits that act to modulate the channel activity. K+Hnov49 is

XX a 4 transmembrane domain, 2 pore domain potassium channel. The gene's

XX chromosomal location is 19q41, determined via PCR chromosomal

XX localisation using primers Z11937 and Z11938. K+Hnov cDNAs

XX were isolated by extension of expressed sequence tags (ESTs) which were

XX related but not identical to known human potassium channels. Potential

XX polymorphisms detected as sequence variants between multiple

XX independent clones. Potassium channels have critical roles in various

CC cell types and biochemical pathways. Defective potassium channels are
 CC known to cause four human diseases: episodic ataxia with myokymia;
 CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
 CC As potassium channels are critical components of virtually all cells,
 CC it is likely that abnormal potassium channels are also implicated in
 CC certain renal, cardiovascular and central nervous system (CNS) disorders.
 CC Nucleotides encoding K-Hnov proteins may be used for identifying
 CC homologous or related proteins and the DNA sequences encoding them. They
 CC may be used to produce compositions that modulate the expression and
 CC function of the K-Hnov protein and in studying the biochemical pathways
 CC associated with it. They may also be used for the recombinant production
 CC of K-Hnov protein in fermentation cultures. Additionally, such
 CC nucleotides may be used in gene therapy protocols for the treatment
 CC of diseases associated with abnormal potassium channels.
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 Ratio: 1.442 Gaps: 9
 Percent Similarity: 51.049 Percent Identity: 24.476

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515 CTGCTGTGACCGCTCAGCCGCGCTTCACCTGCTGTGCTACGTACGT 564
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AC 246092;
XX
DT 05-MAY-2000 (first entry)
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DE cDNA encoding KT4, a TWIK family 2PD potassium channel polypeptide.
XX
KW KT4; TWIK family 2PD potassium channel polypeptide; P-domain;
KW expressed sequence tag; EST; AA604914; ion channel dysfunction;
KW renal disease; musculoskeletal disease; proliferative disease;
KW renal failure; nephrosis; cirrhosis; dysphagia; gastritis; myotonia;
KW muscular dystrophy; atherosclerosis; cancer; ss.
XX
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XX
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XX
PN WO200003687-A2.
XX
PD 27-JAN-2000.
XX
PF 20-JUL-1999; 99MO-US16471.
XX
PR 20-JUL-1998; 98US-0093486.
PR 13-AUG-1998; 98US-0096655.
XX
PA (ELAN-) ELAN PHARM INC.
XX
PI Forsayeth JR, Zhao BB, Chavez RA;
XX
DR WPI: 2000-171196/15.
DR P-PSDB; Y68737.
XX
PT Novel human potassium channel polynucleotides and polypeptides used in
PT the diagnosis, prevention and treatment of diseases including renal
PT failure, cirrhosis, muscular dystrophy and cancers -
XX
XX Claim 14; Fig 1A-C; 53pp; English.
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Date: Mar 17, 2001 7:24 PM
About: Results were produced by the GenCore software, version 4.5.
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; Patent No. 5559026
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; APPLICANT: Pausch, Mark H.
; TITLE OF INVENTION: Functional Expression of a Drosophila
; TITLE OF INVENTION: Melanogaster Putative Potassium Channel in Yeast
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,312
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: P-38,711
; REFERENCE/DOCKET NUMBER: 32,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
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; MOLECULE TYPE: DNA (genomic)
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; NAME/KEY: CDS
; LOCATION: 190..2043
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; Patent No. 6013470
; GENERAL INFORMATION:
; APPLICANT: Lesage, Florian
; APPLICANT: Guillemare, Eric
; APPLICANT: Fink, Michel
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lazdunki, Michel
; APPLICANT: Romey, Georges
; APPLICANT: Barhanin, Jacques
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
; TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
; TITLE OF INVENTION: OF DRUGS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,816
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 183..1190
; US-08-749-816-1

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alignment_scores:
  Quality: 239.00      Length: 263
  Ratio: 1.583         Gaps: 8
  Percent Similarity: 57.414  Percent Identity: 28.137

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alignment_block:

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US-08-816-011c-2 x US-08-749-816-1 ..
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Align seg 1/1 to: US-08-749-816-1 from: 1 to: 1894
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9 LeuLeuIlePheTyrIleSerTyrLeuMetPheGlyAlaAlaIleTyrTy 25
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
258 CTGGCTGGCTGCTACTGTCTACCTGGCTTCTGGCGCAGTGGCTCTCTC 307
25 rHisIleGluHisGlyGluGluLysIleSerArgAlaGluAlaArgLysA 42
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
308 CTCGGTGGAGCTCCCTATGAGACCTGTGCGCCAGGAGCTCGCAAG. 356
42 lacGlnIleAlaIleAsnGluTyrLeuLeuGluGluLeuGlyAspLysAsn 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
357 .....CTGAAGCGACGCTTCTGGAGGAGCAGCAGTGCCTGTCT 395
59 ThrThrGlnAspGluLeuGlnArgIleSerAspTyrCysAsp 75
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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396 GAGCAGCAGCTGGAGCAGTTCTCTGGCGGGTCTCTGGAGCCAGCAACTA 445
75 sProValThrLeuProProThrTyrAspAspThrProTyrThrTrpThr 92
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
446 CGCGGTGTCGGTCTCAGCAACGCCCTCGGCAAC...TGGAACTGGCACT 492
92 heTyrHisAlaPhePhePheAlaPheThrValCysSerThrValGlyTyr 108
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
493 TCACCTCCCGCGCTCTTCTCGCCAGCAGCGTCTCTCCACACAGGTTAT 542
109 GlyAsnIleSerProThrThrPheAlaGlyArgMetIleMetIleAlaTy 125
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
543 GGCACACCGTGCCTTGTGATGAGGAGTAAGGCCTTCGCAATCATCTA 592
125 rSerValIleGlyIleProValAsnGlyIleLeuPheAlaGlyLeuGlyG 142
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
593 CTCGCTCAATTGGCATTCCCTTCACC...CTCCTGTTT 626
142 IuTyrPheGlyArgThrPheGluAlaIleTyrArgArgTyrLysLysTyr 158
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627 .....CTGACGGCTCTGTCTCCAGCGCATCACCGTCAC 659
159 LysMetSerThrAspMetHisTyrValProProGlnLeuGlyLeu..... 173
660 GTCACCCGCGAGCGCGTCTCTACTCCACATCCGCTGGGGCTTCTCCAA 709
174 ....IleThrThrValIleAlaLeuIleProGly.....IleA 186
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710 GCAGGTGGTGGCCATCGTCCATGCCGCTGCTCTGGTTGTCTACCTGT 759
186 laLeuPheLeuValLeuProCysValGlyValHisLeuLeuArgGluLeu 202
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
760 CTTGCTTCTTCTTCTATCCCGCGCTCTCTCTCAGTCTCTGGAGGATGAC 809
203 GlyLeuSerSerIleSerLeuTyrTyrSerTyrValThrThrThrI 219
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
810 TGAACCTCTCTGGAATCCTTTTATTTTGTGTTTCTCTCTGAGCACCAT 859
219 eGlyPheGlyAspTyrValProThrPheGlyAlaAsnGlnProLysGluP 236
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
860 TGGCTGGGGGATTATGTGCTGGGAAGGCTACATAAATAA..... 902
236 heGlyTyrPheValValTyrGlnIlePheValIleValThrPheIle 252
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
903 .....TTCAGAGAGCTCTATAAGATTGGATGATCAGCTGTACCTGCTA 944
253 PheSerLeu...GlyTyrLeuValMetIleMetThrPhe 264
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945 CTGGCCTTATTGCCATGTGGTAGTTCTTGGAAACCTTC 983

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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-332-312-3
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seq_documentation_block:
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; Sequence 3, Application US/08332312
; Patent No. 5559026
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; GENERAL INFORMATION:
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; APPLICANT: Price, Laura A.
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; APPLICANT: Pausch, Mark H.
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; TITLE OF INVENTION: Functional Expression of a Drosophila
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; TITLE OF INVENTION: Melanogaster Putative Potassium Channel in Yeast
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```
; NUMBER OF SEQUENCES: 4
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; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: American Cyanamid Company
```

```
; STREET: One Cyanamid Plaza
```

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; CITY: Wayne
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; STATE: New Jersey
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; COUNTRY: US
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; ZIP: 07470-8426
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: Patent in Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,312
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: P-38,711
; REFERENCE/DOCKET NUMBER: 32,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1008
; US-08-332-312-3

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alignment_scores:
  Quality: 208.50      Length: 344
  Ratio: 1.271        Gaps: 15
  Percent Similarity: 47.674      Percent Identity: 25.291

alignment_block:
US-08-816-011c-2 x US-08-332-312-3
Align seg 1/1 to: US-08-332-312-3 from: 1 to: 1011

89 ThrTrpThrPheTyrHisAlaPhePheAlaPheThrValCysSerTh 105
79 ACATGGACATTTTCATCGCTCCCTTTCTTGGCGTAACCGTCGCATC 128
105 rValGlyTyrGlyAsnIleSerProThrPheAlaGlyArgMetIleM 122
129 CATCGGATACGGTAATCCAGTTCAGTCAGACAAACATTGGACGGAT 178
122 etileAlaTyrSerValIleGlyIleProValAsnGlyIleLeuPhe 138
179 GTATATTGTTCTCCTGTTGGTAATACCTCTAACACTGGTTACCAT 228
139 GlyLeu...GlyGluTyrPheGlyArgThrPheGluAlaIleTyr 154
229 GACTTGGCAGGTAATTCCTATCTGAACATCTCTGTTGGTTGTA 278
154 gTyrLysLysTyrLys..... 159
279 CTATTGGAATTAANAATCTCATATTCTCAGCATCGAAGAAACGGA 328
160 .....MetSerThrAspMet 164
329 GAGAGCAGCTTTGTGAGCACTGTCCACAGTCATGGAATGGGCGCAT 378
165 HisTyrValProGlnLeuGlyLeuIleThrValValIleAlaLe 181
379 AATATGAGGAGAAAGAAATTCCTGCTGTTA..... 414
181 uileProGlyIleAlaLeuPheLeuValLeuProCysValGlyValHis 198
415 .....TTAGCTATTCTGATAGTATATACAGCGCTTTGGCGGTGCC 454
198 euLeuArgGluLeuGlyLeuSerSerIle.....SerLeuTyrTyrSer 212
455 TAATGTCAAAATTAAGACCGGTGGTCTTCTTCACTTCATTCTACTGG 504
213 TyrValThrThrThrIleGlyPheGlyAspTyrValProThrPheG 229
505 TTCATTACAATGACTACTGTGGGGTTTGGGCGACTGTATGCC..... 546

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229 yAlaAsnGlnProLysGluPheGlyTyrPheValValTyrGlnIleP 246
547 .....AGAAGGACGGATACATGTATATCATATGCTCT 580
246 heValIleValTrp.....PheIlePhe 253
581 ATATCATTTTAAAGTAAATTTTCAATGAAAAAACAATAATTCAAA 630
254 SerLeuGlyTyrLeuValMetIleMetThrPheIleThrArgGlyLeu 270
631 TTTTAGGCTTGCATTAACATACTGTCATTGATTGGTAGGAGTACA 680
270 n...SerLysLysLeuAlaTyr..... 276
681 GTATATTCGAAAGATTTCATTATTTCGGAAGAAAAATTCAGACGCT 730
277 .....LeuGluGlnLeuSer 282
731 CTGCATTGGCGTTCTAGGAGGAAGGTAGTCTTGTATCAGAACTCT 780
283 SerAsnLeuLysAlaThrGlnAsnArgIleTrpSerGlyValThrLys 299
781 GCAAAATTA.....ATGCAAAAGCGA..... 801
299 pValGlyTyrLeuArgArgMetLeuAsnGluLeuTyrIleLeuLys 316
802 .....GCTCGTAACATGTCCGAGAGCTTTTATA.....GTGG 835
316 yProValTyrThrAspValAspIleAlaTyrThrLeuProArgSerAsn 332
836 AGAATCTCTATGTTTCCAAACACATCATACCATTCATACCAACTG 885
333 SerCysProAspLeuSerMetTyrArgValGluProAlaProIlePro 349
886 CGATGATTTCGATATATGATCAAACTGCCGATGCTGCTACCATTC 934
349 erArgLysArgAlaPheSerValCys.....AlaAspMetValGly 363
935 ..CGTCATCGTCTGCAATTGATGATGCAAAAGTTGTAGATTTTGC...ATT 979
364 GlnArgGluAlaGlyMetValHisAlaAsn 373
980 CAAGATATTCTCTCAATCGTGCATTCAAAT 1009

seq_name: /cqn2_6/ptodata/2/ina/6_COMB.seq:US-08-650-766-2
seq_documentation_block:
; Sequence 2, Application US/08650766D
; Patent No. 6015690
; GENERAL INFORMATION:
; APPLICANT: PILETZ, John E.
; APPLICANT: IVANOV, Tina R.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND
; FILE OF INVENTION: METHOD FOR CLONING THE SAME
; FILE REFERENCE: Corrected Sequence Listing
; Patent No. 6015690
; CURRENT APPLICATION NUMBER: US/08/650,766D
; CURRENT FILING DATE: 1996-05-20
; EARLIER APPLICATION NUMBER: US 60/012,600
; EARLIER FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 1678
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-08-650-766-2

alignment_scores:
  Quality: 125.50      Length: 332
  Ratio: 0.854        Gaps: 20

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328 LeuProArgSerAsnSerCysProAspLeuSerMet..... 339
    ||| ||||:::|||:::|||::| : ::::
509 CTGCCAGATCATCTCTCGCCCTTCACCTGCATTGGGTACACGCCCACC 558
    340 .TyrArg.ValGluproAlaPro.....IleProSerArgLysArg 352
        ||| ::::::|||:::|||::| :|||::| |||
559 AATCAGACTTCATCCAGCGCTGACGACATGTATCCGGCAGGCCATCGA 608
    353 AlaPheSerValCysAlaAspMet.ValGliValAlaGlnArgGliuAlaGlyM 369
        ||| ::::::|||:::|||::| :|||::| |||::|
609 CGGCGACTGCCTGCCTGGATCGAGGCTGCCAACCGGGGAGGAGGCC 658
    369 etValHisAlaAsnSerAspThrAspLeuThrLysLeuAspArgGluLys 385
        ||| ::::::|||:::|||::| :|||::| |||::|
659 AGGTTGAACAGCGCGCAGGAGGAGGATGAGGAGGAGAAGACAGGAGGAC 708
    386 ThrPheGluThrAlaGluAlaTyrrHisGlnThrThrAspLeuLeuAlaLy 402
        ::: |||
709 GTGGCTGAG..... 717
    402 svaIvalAsnAlaLeuAlaThrValLysProproProAlaGluGinGluA 419
        ||| |||::| :|||::| :|||::| :|||::|
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2352 CCGCACCAGGAGTCTCGGGCAGCACCCAGCACATCCTCTCCT..... 2394
|||||
541 etValCysAspValCysPheProSerArgSerThrProArgArgIle 557
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2395 ..CCCTGCGCTTGTCTTGTTCCTCGCATGCGCAGCTCACCGAGTTG 2442
|||||
558 TrpSerAla.....SerCysProTrp....SerArgTyrProArgValse 571
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2443 GCTTCCTCATGCGGAGCTGTCTGTCTCAAGGTACGGCAGCAGTGA 2492
|||||
571 rSerArgArg.....LysProAspProArgTrpThrThrSerThrA 586
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2493 AACACCTCTTCAATATCTCGGACGCGGCAACCTGCAGGTTCACGC 2542
|||||
586 rg.....SerArgArgProValAsnProIleCys..... 596
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2543 GGACCTGCGCTCATGCTTTGCACCCAGCACATGGCCATGCTGTGTAG 2592
|||||
597 .....AlaThrAspAlaValArgHis..... 603
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2593 CCATCCTCTACGGCAGCCACACAGCTCGAGGAGTCTCGGCCAGCTG 2642
|||||
604 .ArgProSerAsnArgMetAlaAlaAlaAlaAla 616
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2643 CTCACCTTCTACAAG.....TGGTGGCGGCTGCC 2673
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:us-08-922-635-3

seq_documentation_block:

; Sequence 3, Application US/08922635A

; Patent No. 6033871

; GENERAL INFORMATION:

; APPLICANT: PILETZ, John E.

; APPLICANT: IVANOV, Tina R.

; TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES

; TITLE OF INVENTION: AND POLYPEPTIDES ENCODED THEREBY

; FILE REFERENCE: Corrected Sequence Listing

; Patent No. 6033871

; CURRENT APPLICATION NUMBER: US/08922.635A

; CURRENT FILING DATE: 1997-09-03

; EARLIER APPLICATION NUMBER: 08/650,766

; EARLIER FILING DATE: 1996-05-20

; EARLIER APPLICATION NUMBER: 60/012,600

; EARLIER FILING DATE: 1996-03-01

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 3318

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-08-922-635-3

alignment_scores:

Quality: 125.50

Ratio: 0.854

Percent Similarity: 44.277

Length: 332

Gaps: 20

Percent Identity: 25.301

alignment_block:

US-08-816-011c-2 x US-08-922-635-3 ..

Align seg 1/1 to: US-08-922-635-3 from: 1 to: 3318

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1873 CTGCGCAGATCATCTTCTGCGCTTCCATTCGCTACGGCCACC 1922

340 .TyrArg.ValGluProAlaPro.....IleProSerArgLysArg 352

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

1923 AATCAGGACTTATCCAGCGCTGAGCACACTATCCGGCAGGCCATCGA 1972

353 AlaPheSerValCysAlaAspMet.ValGlyAlaGlnArgGluAlaGlyM 369

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1793 CCGCGAGCTGCTCTGCTGATCGAGGTGCCAACCCAGCGGAGGAGGCC 2022
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
369 etValHisAlaAsnSerAspThrAspLeuThrLysLeuAspArgGluLys 385
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2023 AGGTTAACAACAGCGCGAGGAGGATGAGGAGGAGGAGGAGGAGGAGG 2072
|||||
386 ThrPheGluThrAlaGluAlaTyrHisGlnThrThrAspLeuLeuAla 402
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2073 TGGCTGAG..... 2081
|||||
402 sValValAsnAlaLeuAlaThrValLysProProAlaGluGlnGluA 419
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2082 .....AACCGTACTTTGAAATGGGCCCCCAGCAGCTGGAGGAGGAGG 2124
|||||
419 spAlaAlaLeuTyrGlyTyrHisGlyPheSerAspSerGlnIleLeu 435
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2125 AG.....GGAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2156
|||||
436 AlaSerGluTrpSerPheSerThrValAsnGluPheThrSerProArg 452
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2156 ..... 2156
|||||
452 gProArgAlaArgAlaCysSerAspPheAsnLeuGluAlaProArgTrp 469
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2157 .....GAGAGG 2163
|||||
469 InSerGlu.ArgProLeuArgSerSerHisAsnGluTrpThrTrpSer 485
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2164 AGGATCAAGAGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2204
|||||
485 yAspAsnGlnGlnIleGlnGluAlaPheAsnGlnArgTyrLysGlyGln 502
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|||||
502 InArgAlaAsnGlyAla.....AlaAsn 509
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2252 CAAGGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2301
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510 SerThrMetValHisLeuGluProAspAlaLeuGluGluGlnLeuArg 526
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2302 TCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2351
|||||
526 nAsnHisArgVal.....ProValAlaSerArgSerSerProCysArg 541
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2352 CCGCACCAGGAGTCTCGGGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2394
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541 etValCysAspValCysPheProSerArgSerThrProArgArgIle 557
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2395 ..CCCTGCGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 2442
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558 TrpSerAla.....SerCysProTrp....SerArgTyrProArgVal 571
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2443 GCTTCCTCATGCGGAGCTGTCTGTCTCAAGGTACGGCAGCAGTGA 2492
|||||
571 rSerArgArg.....LysProAspProArgTrpThrThrSerThrA 586
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2493 AACACGCTTCTTATATCTCGGACGCGGCCAACCTGCACGAGTTCACGC 2542
|||||
586 rg.....SerArgArgProValAsnProIleCys..... 596
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2543 GGACCTGCGCTCATGCTTTGCACCCAGCACATGGCCATGCTGTGTAG 2592
|||||
597 .....AlaThrAspAlaValArgHis..... 603
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2593 CCATCCTCTACGGCAGCCACACAGCTCGAGGAGTCTCGGCCAGCTG 2642
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604 .ArgProSerAsnArgMetAlaAlaAlaAlaAlaAla 616
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2643 CTCACCTTCTACAAG.....TGGTGGCGGCTGCC 2673
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:us-08-650-766-1

seq_documentation_block:
 ; Sequence 1, Application US/08650766D
 ; Patent No. 6015690
 ; GENERAL INFORMATION:
 ; APPLICANT: PILETZ, John E.
 ; APPLICANT: IVANOV, Tina R.
 ; TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND METHOD FOR CLONING THE SAME
 ; FILE REFERENCE: Corrected sequence Listing
 ; Patent No. 6015690
 : CURRENT APPLICATION NUMBER: US/08/650,766D
 : CURRENT FILING DATE: 1996-05-20
 : EARLIER APPLICATION NUMBER: US 60/012,600
 : EARLIER FILING DATE: 1996-03-01
 : NUMBER OF SEQ ID NOS: 21
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 1
 : LENGTH: 3385
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (1398)..(3383)
US-08-650-766-1

alignment_scores:

Quality: 125.50 Length: 332

Ratio: 0.854 Gaps: 20

Percent Similarity: 44.277 Percent Identity: 25.301

Alignment seg 1/1 to: US-08-650-766-1 from: 1 to: 3385

US-08-816-011C-2 x US-08-650-766-1 ..

alignment_block:

328 LeuProArgSerAsnSerCysPheValAlaGluLeuMet..... 339
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340 TyrArg.ValGlutProAlaPro.....IleProSerArgLysArg 352
||| :::::::::::::::::::: ||| |
1956 AATCAGCACTTCATCCAGCCCTTGACACACTGATCCGCGCACGACATCGA 2005
353 AlaPheSerValCysAlaAspMet.ValGlyAlaGlnArgGluAlaGlyM 369
||| :::::::::::::::::::: ||| |
2006 CGCGCAGCTGCTGCTGGATCGAGGCTGCCAACACCGAGGAGGAGGCC 2055
369 etValHisAlaAsnSerAspThrLysLeuAspArgGluLys 385
::: :::::::::::::::::::: ||| ::
2056 AGGGTGAACAGCGGAGGAGGAGGAGGAGGAGAAGAGGAGGAC 2105
386 ThrPheGlnThrAlaGluAlaTyrlHisGlnThrThraspleuLeuAlaLy 402
::: ||| |
2106 GTGGCTGAG..... 2114
402 svaValAsnAlaLeuAlaThrVallysProproAlaGluGlnGluA 419
||| :::::::::::::::::::: ||| |
2115AACGGCTACTTGAATGGGGCCCCCAGCAGCTGGAGGAGGAGG 2157
419 spAlaAlaLeuTyrgltyrHisglyPheSerSerpSerGlnlleLeu 435
:: ||| |
2158 AG.....GGAGGAGGCGGAGGAGGAGGAGGAGGAG..... 2189
436 AlaserGluTrpSerPheSerThrValAsnGluPhetrhrSerProArgAr 452
2189 2189
452 gProArgAlaArgAlaCysSerAspPheAsnLeuGluAlaProArgTrpg 469
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2190GAAAGG 2196

[illegible]

188PheLeuValLeuPro.....CysValGlyValHisLeuLe 199
3677 GATCAGCTGTCTCTGCTGTGCTCCCAACCACTGT..... 3709
199 uArgGluLeuGlyLeuSerSerLeuLeuTyrTyrSerTyrValThr. 215
3710CTGGGATGGAGTACAGAGTCTTACGAGAACTACGAGACGC 3752
216ThrThrIleGlyPheGlyAspTyrValProThrPhe 228
3753 GGAGGTACTGCACCTCTCCGAGGTCCGCGCCCACTACTGCAAGAAATAT 3802
229 GlyAlaAsnGlnProLysGluPheGlyTyrTrpPheValVal....TyrG1 244
3803 AACATCAGTACAGGAGCACTTCTATGCTGGAGCGCCCGGGGTCGG 3852
244 nIlePheValIleValTrpPheIlePheSerLeuGlyTyrLeuValMetI 261
3853 CCGGTTTGGCTCCTCATGCCGCCCTCAGGGTCGGCTACCTCATCTCTGC 3902
261 leMetThrPheIleThrArgGlyLeuGlnSerLysLysLeuAlaTyrLeu 277
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278 GluGlnGlnLeuSerSerAsnLeuLysAlaThrGlnAsnArgIleTrpSe 294
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seq_documentation_block:
; Sequence 24, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IGS-9.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..5053
; US-08-762-500-24

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alignment_scores:
  Quality: 124.50      Length: 596
  Ratio: 0.454        Gaps: 34
  Percent Similarity: 45.973  Percent Identity: 22.148

alignment_block:
US-08-816-011c-2 x US-08-762-500-24
Align seg 1/1 to: US-08-762-500-24 from: 1 to: 5894

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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:us-08-447-965A-1
seq_documentation_block:
; Sequence 1, Application US/08447965A
; Patent No. 5776692
; GENERAL INFORMATION:
; APPLICANT: El-Zaatari, Fouad A. K.
; APPLICANT: Naser, Saleh
; TITLE OF INVENTION: Mycobacterial Genus-Specific DNA Probe
; NUMBER OF INVENTION: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fulbright & Jaworski L.L.P.
; STREET: 801 Pennsylvania Ave. N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Davis, Peter J.
; REGISTRATION NUMBER: 36,119
; REFERENCE/DOCKET NUMBER: 311.019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-662-4669
; TELEFAX: 202-662-4643
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
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US-08-447-965A-1

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Quality: 124.00 Length: 349
Ratio: 0.832 Gaps: 18
Percent Similarity: 42.693 Percent Identity: 25.788

alignment_block:

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seq_name: /cgn2_6/ptodata/2/lna/6_COMB.seq:US-08-510-646B-17

seq_documentation_block:

; Sequence 17, Application US/08510646B
; Patent No. 6077699

GENERAL INFORMATION:

; APPLICANT: Blanc, Veronique
; APPLICANT: Blanc, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie

TITLE OF INVENTION: Polypeptides Involved In The

TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences

TITLE OF INVENTION: Coding For These Polypeptides And Their Use

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/510,646B

FILING DATE: 03-AUG-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/403,852

FILING DATE: 10-MAY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR 93/00923

FILING DATE: 25-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 92/11441

FILING DATE: 25-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03806.0054-01000

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000
 ; TELEFAX: (202) 408-4400
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2219 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: genomic DNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: S. virginiae
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..2219
 ; OTHER INFORMATION: /product = "virginiamicin s synthase gene"
 ; US-08-510-646B-17

alignment_scores:

Quality: 123.50 Length: 318
 Ratio: 0.908 Gaps: 18
 Percent Similarity: 42.767 Percent Identity: 25.472

alignment_block:

US-08-816-011c-2 x US-08-510-646B-17 ..

Align seg 1/1 to: US-08-510-646B-17 from: 1 to: 2219

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317 ProValTyrThrAspValAspIleAlaTyrThrLeuProArgSerAsnSe 333
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
552 CCACTACCGCGACCTACCGCGGCTTACACCGCGCGCGCGCGCGGCG 601
333 rCysProAspLeuSerMetTyrArgValGluProAlaProIleProSerA 350
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
602 CGCCCCCGACTGG.....GAGCCCTCCCGGTCCAG.... 632
350 rGlyArgAlaPheSerValCysAlaAspMetValGlyAlaGlnArgGlu 366
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
633 .....TACCGCGACTACACCTCTGGCAGCAGGAG 662
367 AlaGlyMetValHisAlaAsnSerAspThrAspLeuThrLysLeuAspAr 383
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
663 .....ATGCTCGGCTCGCGGACGACCGCGAC..... 689
383 gGluLysThrPheGluThrAlaGluAlaTyrHisGlnThrThrAspLeuL 400
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
690 .....AGCTCGGCGCCCGCCAGCTCGACCACTGGCGCCCGGTCCCTGG 732
400 eu.AlalysValValasn.....AlaLeuAlaThrValLysPr 412
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
733 CCGGCGCCCGCGAGCACTGGAACTGCCACCGACCGACACACCGCGCGCC 782
412 oProProAlaGluGlnGlu.....AspAlaAlaL 422
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
783 GCCCGCGCCACCAACCGCGCCCGCTCCCTTCCACCTGGAGCCCGAGCT 832
422 euTyrGlyGlyTyrHisGlyPheSerAspSerGlnIleLeuAlaSerGlu 438
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
833 GCACGAGCGGCTCAGCGCCCTGGCCAGGTCTCGGACGCCAGCCTGTCA 882
439 TrpSerPheSerThrValAsnGluPheThrSerProArgArgProArgAl 455
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
883 TGTGCC.....TGCACGCGCGGTTCGCCGCGC.. 909
455 aArgAlaCysSerAspPheAsnLeuGluAlaProArgTyrGlnSerGluA 472
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
910 .....TGCTCAACAGCAGGTGCGCGGACCGACCATCCGATCGGCGAG 952
472 rGPro.....LeuArgSer 476
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
953 CCCCATCGCGCGCGCACCGACGAGGCCCTCGACGATCTGTCGGGTCT 1002

```

```

477 SerHisAsnGluTyrThrTrpSerGlyAspAsnGlnGlnIleGlnGluAl 493
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1003 TCGTCAACACCTGGTCTGCGCACCGACACCTCCGGCGATCCGACCTTC 1052
493 aPheAsnGlnArgTyrLysGlyGlnArgAlaAsnGlyAlaAlaAsnS 510
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1053 CGCGAACTCGTGGCAC.....GCACCGCGCGCAC 1081
510 erThrMetValHisLeuGluProAspAlaLeuGluGlnLeuArgAsn 526
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1082 CGACCTGGCGCATACGACACCGAGGACCTGCCCTTCG.....AGAAGC 1125
527 AsnHisArgValProValAlaSerArgSerProCysArgMetValCy 543
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1126 TCGTCGAGACTCTCAACCGCGAGCGCTCGCTCGCCGCAACCCGCTGTC 1175
543 sAspValCysPheProSerArgSerThrProArgArgIleTrpSerA 560
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1176 CAGGTACTGTGGCTTCC...AGAGCATGCCACGCGAC.....AGCC 1216
560 laSerCysProTrpSer.ArgTyrProArgValSerSerArgArg..... 574
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1217 CGTGTGCCCGGCTCGACGTCTCCAGCGGCGGCTCGCGCTCGATTTCG 1266
575 .....LysProAspProArgTrpThrThrSerThrArgSerArgA 589
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1267 CCAAGTTCGACCTGGCCCT...GGCCGTGGCGGAGGACGCGACCGCGAC 1313
589 rgProProValAsnProIleCysAlaThrAspAlaValArgHisArgPro 605
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1314 GGCGCGCGGTC.....GCTCGCGGCGGACTGGGAGTTACGACCGGACCT 1357

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OM of: US-08-816-011c-2 to: EST.* out_format : pfs
Date: Mar 17, 2001 6:53 PM
About: Results were produced by the GenCore software, version 4.5.
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters: -MODEL-frame+ p2n.model -DEV=xlip
-Q/cgn2/_JUSPTO_spool/US08816011/runat_07032001_122538_23497/app_query.fasta_1.686
-DB-EST -QFMT-fastap -SUFFIX=fst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -CGAPOP=4.500
-CGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-FGAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXI=7.000 -START=1 -MATRIX=blomsu62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM-ext -MINLEN=0
-MAXLEN=2000000000 -USER=US08816011 @CGN1_1.2753 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-08-816-011c-2
Query length: 618
Database: EST.*
Database sequences: 7991742
Database length: 791223438
Search time (sec): 885.420000

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
gb_est8:AA539933	+ 657.00	1048.42	2.2e-49	582	! AA539933 LD19236.5prime LD Dros
gb_est20:AI405401	+ 579.00	924.33	1.8e-42	487	! AI405401 GH25390.5prime GH Dros
gb_est74:BE680493	+ 234.00	363.92	2.9e-11	586	! BE680493 df81b01.y1 Xenopus lae
gb_est22:AI605559	+ 232.50	359.78	5.0e-11	677	! BE680559 ms07h04.y1 Soares mous
gb_est45:AW506290	+ 228.00	352.61	1.3e-10	671	! AW506290 GEL674 Globodera rostr
gb_est70:BE377948	+ 207.00	319.98	8.2e-09	599	! BE377948 601230123F1 NCI_CGAP_M
gb_est27:AI956397	+ 202.00	310.45	2.8e-08	676	! AI956397 ul74g06.y1 Sugano mous
gb_est19:AI325858	+ 193.50	300.69	9.8e-08	483	! AI325858 mf89d07.y1 Soares mous
gb_est37:AV612885	+ 186.50	286.65	5.9e-07	607	! AV612885 AV612885 MS taurus lu
gb_est78:BE981482	- 184.00	282.94	9.5e-07	590	! BE981482 UT-M-CG0p-bdb-f-10-0-0
gb_est78:BE981393	- 183.00	281.27	1.2e-06	593	! BE981393 UT-M-CG0p-bdb-f-11-0-0
gb_est7:AA64375	+ 175.50	273.78	3.1e-06	401	! AA64375 zx8ld11.rl Soares ovari
gb_est47:AW644141	+ 175.00	267.56	6.8e-06	632	! AW644141 cm37h06.w1 blackshear/
gb_est69:BE309179	+ 171.00	259.19	2.0e-05	742	! BE309179 601095044F1 NCI_CGAP_M
gb_est27:AI956401	+ 170.00	258.68	2.1e-05	676	! AI956401 ul74g11.y1 Sugano mous
gb_est27:AI956216	+ 169.50	257.76	2.4e-05	682	! AI956216 ul72g10.y1 Sugano mous
gb_est38:AW012076	+ 165.00	253.01	4.4e-05	551	! AW012076 um07e02.y1 Sugano mous
gb_est70:BE377443	+ 165.00	250.50	6.1e-05	681	! BE377443 601228920F1 NCI_CGAP_M
gb_gss26:CN5033Y1	- 159.00	236.13	0.0004	1008	! AL2293347 Tetraodon nigroviridi
gb_est19:AI327069	- 156.50	237.56	0.0003	636	! AI327069 mf89d07.x1 Soares mous
gb_est39:AW042072	+ 153.50	233.30	0.0006	605	! AW042072 SWL4CAK03E08SK Brugla
gb_est19:AI391151	+ 151.50	232.16	0.0006	507	! AI391151 mcl6h08.y1 Soares mous
gb_est73:BE735881	+ 151.50	224.82	0.0016	941	! BE735881 601305237F1 NIH_MGC_39
gb_gss26:CN5031QR	+ 147.00	216.58	0.0047	1020	! AL223884 Tetraodon nigroviridi
gb_est8:AA533124	+ 144.00	224.09	0.0018	360	! AA533124 nj46f11.s1 NCI_CGAP_P
gb_est87:AW99136	+ 139.50	218.28	0.0038	318	! AW99136 mf89d07.rl Soares mous
gb_est48:AW701618	+ 138.50	208.85	0.0127	614	! AW701618 uc68d11.y1 NCI_CGAP_Lu
gb_est41:AW227291	+ 134.50	204.91	0.0211	496	! AW227291 uc66g11.y1 Sugano mous
gb_est71:BE466893	+ 133.00	207.08	0.0160	337	! BE466893 hz28d11.x1 NCI_CGAP_GC
gb_est27:AI968607	+ 133.00	204.02	0.0237	436	! AI968607 wt90e12.x1 NCI_CGAP_GC
gb_est23:AI690321	+ 133.00	203.46	0.0234	457	! AI690321 tz15905.x1 NCI_CGAP_UT
gb_gss26:CN502FUC	- 131.00	191.88	0.1122	923	! AI95501 Tetraodon nigroviridis
gb_est69:BE284810	+ 129.50	199.03	0.0449	412	! BE284810 601091118F1 NCI_CGAP_M
gb_est49:AW784337	+ 125.50	192.30	0.1063	421	! AW784337 z661d11.g1 Canis cDNAs
gb_est23:AI678413	+ 125.00	194.03	0.0852	340	! AI678413 tu81h10.x1 NCI_CGAP_Ga
gb_est24:AI739096	+ 125.00	193.09	0.0961	368	! AI739096 w117h03.x1 NCI_CGAP_Co
gb_est66:BE083884	- 125.00	191.60	0.1163	417	! BE083884 CM0-BY0687-210300-297-
gb_gss26:CN50209Q	+ 124.50	181.62	0.4183	903	! AL214199 Tetraodon nigroviridis
gb_est44:AW429512	+ 123.50	189.64	0.1495	401	! AW429512 67771 MARC iPig Sus sc
gb_est80:D35319	+ 123.00	190.11	0.1407	360	! D35319 BELK01904F Yuji Kohara u
gb_est40:AW141881	+ 123.00	185.25	0.2625	542	! AW141881 EST291996 Normalized

gb_est74:BE720244 + 121.50 183.36 0.3344 518 ! BE720244 RCO-HT0885-080800-0
gb_est70:BE405216 - 121.00 181.11 0.4465 585 ! BE405216 WHE1211_B04_D072S W
gb_est75:BE734519 - 121.00 176.83 0.7732 839 ! BE734519 601570611F1 NIH_MGC
gb_est47:AW660458 + 120.50 181.19 0.4422 543 ! AW660458 98514 MARC 1BOV Bos
seq_name: gb_est8:AA539933
seq_documentation_block: 582 bp mRNA EST 27-NOV-1998
LOCUS AA539933 LD19236.5prime LD Drosophila melanogaster embryo Bluescript
DEFINITION Drosophila melanogaster cDNA clone LD19236 5prime, mRNA sequence.
ACCESSION AA539933
VERSION AA539933.1 GI:2795149
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 582)
AUTHORS Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein
,P., Lewis,S. and Rubin,G.M.
TITLE BDGP/HIMI Drosophila EST Project
JOURNAL Unpublished (1997)
COMMENT On Jan 19, 1998 this sequence version replaced gi:2286367.
Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Plate: 192 row: C column: 12
High quality sequence stop: 429.
FEATURES
Location/Qualifiers
source 1..582
/organism="Drosophila melanogaster"
/db_xref="BDGP-EST:BDcin018335"
/db_xref="taxon:7227"
/clone="LD19236"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
/note="organ: embryo; Vector: Bluescript SK; Site:1: EcoRI
Site:2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis kit. Oligo dt-primed and directionally cloned at
EcoRI and XhoI in Bluescript SK(+/-)"
BASE COUNT 154 a 145 c 131 g 151 t 1 others
ORIGIN

alignment_scores:
Quality: 657.00 Length: 124
Ratio: 5.298 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.387
alignment_block:
US-08-816-011c-2 x AA539933
Align seg 1/1 to: AA539933 from: 1 to: 582
1 MetSerProAsnArgTrpIleLeuLeuLeuIlePheTyrIleSertYrle 17
|||||
210 ATGTCGCCGAATCGATGATCGCTCTCATCTTCTACATATCTTCTACT 259
17 uMetPheGlyAlaAlaIleTyrTyrHisIleGluHisGlyGluGluLysI 34
|||||
260 GATGTCGGCGCGCAATCTATTACCATATTGACGACGCGGAGGAGA 309
34 leSerArgAlaGluGlnArgLysAlaGlnIleAlaIleAsnGluTyrIle 50
|||||
310 TATCGCGCGCGCAACGCGCAAGCGCAATGCAATCAACGAATATCTG 359

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51 LeuGluGluLeuGlyAspLysAsnThrThrThrGlnAspGluIleLeuG1 67
|||||
360 CTGGAGGAGCTGGGGACAAGAATACGACCACACAGGATGAGATTCTTCA 409
|||||
67 nArgileSerAspTyrCysAspLysProValThrLeuProProThrTyrA 84
|||||
410 ACGGATCTCGGATTACTGTGACAACCGGTTACATGCGCGGACATATG 459
|||||
84 spAspThrProTyrThrTrpThrPheTyrHisAlaPhePheAlaPhe 100
|||||
460 ATGATACGCCCTTACACGTTGACCTTCTACCATGCTTCTTCTCGCCTTC 509
|||||
101 ThrValCysSerThrValG1G1TyrGlyAsnIleSerProThrThrPheAl 117
|||||
510 ACCGTTTCTCCTCACGGTGGGATATGCAATATATCGCAACACCCTTCGC 559
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117 aGlyArgMetIleMetIleAla 124
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560 CGGACGGATGATTCTGATCGCG 581
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seq_name: gb_est20:AI405401

seq_documentation_block:
LOCUS AI405401 487 bp mRNA EST 08-FEB-1999
DEFINITION GH25390.5prime GH Drosophila melanogaster head pOT2 Drosophila
melanogaster cDNA clone GH25390 5prime similar to U55321: Ork1
P8gn0017561 PID:g1666503 SPTREMBL:Q94526, mRNA sequence.
ACCESSION AI405401
VERSION AI405401.1 GI:4248488
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyceta;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 487)
AUTHORS Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein
, P., Lewis, S. and Rubin, G.M.
TITLE BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539r USA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 253 row: H column: 6
High quality sequence stop: 413.
Location/Qualifiers
1..487
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH25390"
/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site:1: EcoRI; Site:2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
BASE COUNT 102 a 155 c 148 g 82 t
ORIGIN

alignment_scores:
Quality: 579.00 Length: 111
Ratio: 5.312 Gaps: 1
Percent Similarity: 98.198 Percent Identity: 96.396

alignment_block:
US-08-816-011c-2 x AI405401
Align seg 1/1 to: AI405401 from: 1 to: 487

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509 AsnSerThrMetValHisLeuGluProAspAlaLeuGluGlnLeu.A 525
|||||
3 AACTCGACCATGGTCCATCTGGAGCGGATGCTTTGGAGGAGCAGCTGAA 52
|||||
525 rGAsnAsnHisArgValProValAlaSerArgSerSerProCysArgMet 541
|||||
53 GAAACAATCACCGGTGCGGTCGCGTCAAGAAGTTCTCCCATGCCGGATG 102
|||||
542 ValCysAspValCysPheProSerArgSerThrProArgArgIleTr 558
|||||
103 GTCGCGACGCTGCTTTCCCTTCAGAAAGCGCCCTCCAGGATCTG 152
|||||
558 pSerAlaSerCysProTrpSerArgTyrProArgValSerSerArgArgL 575
|||||
153 CAGCGCAAGTTGTCGCTGCTCGGTACCCGAGGCGTGTCTCATCTCGCAGCA 202
|||||
575 ysProAspProArgTrpThrThrSerThrArgSerArgArgProPro 591
|||||
203 AGCCAGATCCCGCTGGACTACTACAGCACACGCTCACGGCGGCTCCA 252
|||||
592 ValAsnProIleCysAlaThrAspAlaValArgHisArgProSerAsnAr 608
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253 GTCATCTCTATTGGCGAACGACGCGGTCCGCCACCGCCCTTCGATCG 302
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608 gMetAlaAlaTrpProAlaAlaAlaAlaGly 618
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303 AATGGCAGCTTGGCAGCGGCGCGCGCGGC 333
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seq_name: gb_est74:BE680493

seq_documentation_block:
LOCUS BE680493 586 bp mRNA EST 11-SEP-2000
DEFINITION df81b01.y1 Xenopus laevis oocyte non normalized xenopus laevis cDNA
clone XENOPUS_SOURCE_ID:xlnnoc002m02 5' similar to TR:095279 095279
TWO PORE DOMAIN K+ CHANNEL. ;, mRNA sequence.
ACCESSION BE680493
VERSION BE680493.1 GI:10064401
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 586)
AUTHORS Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
, Martin, J., Wylie, I., Underwood, K., Theising, B., Bowers, Y., Person
, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
Waterston, R. and Wilson, R.
WashU Xenopus EST project, 1999
Other_ESTs: df81b01.x1
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
below when ordering this clone: Source lab clone id - xlnnoc002m02
Seq primer: -40RP from Gibco
High quality sequence stop: 426.
Location/Qualifiers
1..586
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XENOPUS_SOURCE_ID:xlnnoc002m02"
FEATURES
Source

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  Ratio: 1.788
  Percent Similarity: 58.036
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High quality sequence stop: 450.
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 /sex="unknown"
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 /dev_stage="13.5-14.5dpc total fetus"
 /lab_host="DH10B"
 /note="Vector: p773D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTTCACCAATCGAAGTCGGCGCGCGCGGAAATTTTTTTTTTTTTT
 T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
 State Univ., from 2]; double-stranded cDNA was ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 pT73 vector. Library went through one round of
 normalization, and was constructed by Bento Soares and
 M. Fatima Bonaldo."

BASE COUNT 82 a 160 c 137 g 104 t
 ORIGIN

alignment_scores:
 Quality: 193.50 Length: 138
 Ratio: 2.224 Gaps: 3
 Percent Similarity: 63.043 Percent Identity: 30.435

alignment_block:
 US-08-816-011c-2 x AI325858 ..

Align seg 1/1 to: AI325858 from: 1 to: 483

90 TrpThrPheTyrHisAlaPhePheAlaPheThrValCysSerThrVa 106
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 37 TGGCGCTCGCGGCTCTTCTACTTCGCCATCACCGTCATCACCAT 86
 106 lGlyTyrGlyAsnIleSerProThrPheAlaGlyArgMetIleMetI 123
 :|||:|||||: :|||:||||| :|||:|||||: :|||: |||:
 87 CGCTATGTCTATCGCGCGCCCGCCAGCAGCGAGGAGGTCTTGCA 136
 123 leAlaTyrSerValIleGlyIleProValAsnGlyIleLeuPheAlaGly 139
 :|||:|||||: :|||:||||| :|||:|||||: :|||: |||:
 137 TGTCTACGGCTGCTGGGCTATCCGCTCACACTAGTCTCCAGAGC 186
 140 LeuGlyGluTyrPheGlyArgThrPheGluAlaIleTyrArgTyrLy 156
 ||| ||| :|||: |||: |||: |||: |||: |||: |||:
 187 CTGGTGAAGCATCAAC.....ACCTCTGTGAGGTACCT 221
 156 sLysTyrLysMetSerThrAspMetHisTyrValProGlnLeuGlyL 173
 :|||: |||: :|||: |||: :|||: |||: :|||: |||:
 222 GCTGCACCGTGCAGAGGGGCTGGGCGATGCGGCACCGCGAGGTGCCA 271
 173 eutIleThrValValIleAlaLeuIleProGlyIleAlaLeuPheLeu 189
 :|||: |||: :|||: |||: :|||: |||: :|||: |||:
 272 TGGCCACATGGTCTCATCGGTTTCTGTCGTGCATCAGCAGCTG... 318
 190 ValLeuProCysValGlyValHisLeuLeuArg.....GluLeuGlyLe 204
 ||| ||| :|||: |||: |||: |||: |||: |||: |||:
 319TGCATCGGCGAGCTGCTCTCTACTACGAGCGCTGGAC 359
 204 uSerSerIleLeuTyrTyrSerTyrValThrThrThrIleGlyP 221
 :|||: |||: :|||: |||: :|||: |||: :|||: |||:
 360 TTTCTTCCAGGCTATTACTACTGCTTCTTCTTCTTCTTCTTCTTCT 409
 221 heGlyAspTyrVal 225
 ||| ||| :|||: |||: |||: |||: |||: |||: |||:
 410 TCGCGCACTATG 423

seq_name: gb_est37:AV612885
 seq_documentation_block: 607 bp mRNA EST 30-AUG-2000
 LOCUS AV612885 Bos taurus lung fetus Bos taurus cDNA clone ELLU048D11 5',
 DEFINITION AV612885 Bos taurus lung fetus Bos taurus cDNA clone ELLU048D11 5',
 mRNA sequence.
 ACCESSION AV612885
 VERSION AV612885.1 GI:9748555
 KEYWORDS EST.
 SOURCE COW.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 607)
 AUTHORS Sugimoto,Y., Hirotsume,S., Takasuga,A., Itoh,R., Jitohzono,A. and
 Suzuki,H.
 TITLE bovine cDNA sequencing
 JOURNAL unpublished (2000)
 COMMENT Contact: Yoshikazu Sugimoto
 Animal Genetics Division
 Shirakawa Institute of Animal Genetics
 Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
 Tel: 81-248-23-5641
 Fax: 81-248-25-5725
 Email: kazusugi@coo.ocn.ne.jp
 Single pass sequencing.
 This clone was obtained from a polyA-deleted cDNA library.
 FEATURES
 Location/Qualifiers
 1..607
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone="ELLU048D11"
 /clone_lib="Bos taurus lung fetus"
 /tissue_type="lung"
 /dev_stage="fetus"
 /lab_host="DH10B"
 /note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
 was deleted from a NotI site"
 BASE COUNT 118 a 184 c 148 g 157 t
 ORIGIN

alignment_scores:
 Quality: 186.50 Length: 184
 Ratio: 1.759 Gaps: 6
 Percent Similarity: 57.609 Percent Identity: 29.891

alignment_block:
 US-08-816-011c-2 x AV612885 ..

Align seg 1/1 to: AV612885 from: 1 to: 607

88 TyrThrTrpThrPheTyrHisAlaPhePheAlaPheThrValCys 104
 :|||: |||: :|||: |||: :|||: |||: :|||: |||:
 24 TGGAACTGGGACTTCACCTCGCGGCTCTTCTGCGCAGCACCGTGTCTC 73
 104 rThrValGlyTyrGlyAsnIleSerProThrThrPheAlaGlyArgMetI 121
 ||| ||| :|||: |||: |||: |||: |||: |||: |||:
 74 CACCAAGGTTACGGATCACACCGTGGCTGTCCGACGGGGGCAAGGCT 123
 121 leMetIleAlaTyrSerValIleGlyIleProValAsnGlyIleLeuPhe 137
 :|||: |||: :|||: |||: :|||: |||: :|||: |||:
 124 TCTGCATCATCTATTCGTCTATCGGATACCTTTTCACC...CTTCTGTT 170
 138 AlaGlyLeuGlyGluTyrPheGlyArgThrPheGluAlaIleTyrArg 154
 :|||: |||: :|||: |||: :|||: |||: :|||: |||:
 171CTGAGGCGAGTGGTCCAGCG 190
 154 gTyrLysLysTyrLysMetSerThrAspMetHisTyrValProGlnL 171
 :|||: |||: :|||: |||: :|||: |||: :|||: |||:
 191 TGTACCATCATGTACCGCGAGCGAGTCTCTACTTCTCCAGTCCGCT 240

ORGANISM

Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 632)
Blackshear,P.J., Lai,W.S., Thorn,J.M., Kennington,E.A., Staffa,N.G.
Jr., Moore,D.T., Bouffard,G.G., Beckstrom-Sternberg,S.M., Touchman
J.W., Bonaldo,M.F. and Soares,M.B.
The NIEHS Xenopus Maternal EST Project
Unpublished (2000)
Contact: Parry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
USA
Tel: 919 541-4899
Fax: 919 541-4571
Email: black009niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
cdna@resgen.com
DNA Sequencing and analyses performed by National Institutes of
Health Intramural Sequencing Center (NISC).
PCR Primers
FORWARD: TGTAAGACGACGCGCCAGT
BACKWARD: CAGGAACAGCTATGACC
Plate: 0136 row: H column: 06
Seq primer: T7 primer.
Location/Qualifiers
1..632
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="PBX0136H06"
/clone_lib="Blackshear/Soares normalized Xenopus egg
library"
/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
/note="Vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-dT18 primer; double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pT7T3-Pac vector.
The library contained approximately 7.2 X 10⁵
recombinants, with average insert sizes of 1-1.5 kb."

FEATURES

source

BASE COUNT

ORIGIN

alignment_scores:

Quality:

Ratio:

Percent Similarity:

alignment_block:

US-08-816-011C-2 x AA464375

Align seg 1/1 to: AA464375 from: 1 to: 401

58 AsnThrThrThrGlnAspGluLeuGlnArgIleSerAspTyrCysAs 74

9 AATTCGACGGAGCTGGATGAAGTCACTCAGCAATATAGTGGCAGCAATAAA 58

74 pLys.....ProValThrLeuProProThrTyrAspThrProT 88

59 TGCAGGGATTATACCGTTAGAAACACCTCCAATCAATCACT 100

88 yrThrThrThrPheThrHisAlaPhePheAlaPheThrValCysSer 104

101 ..CACTGGGATTTGGGAAGTTCCCTCTCTCTGCTGGCACTGTTATTACA 148

105 ThrValGlyTyrGlyAsnIleSerProThrThrPheAlaGlyArgMetII 121

149 ACCATAGATTGGAAACATCTCACACGACACAGCGGCAAAATTT 198

121 eMetIleAlaTyrSerValIleGlyIleProValAsnGlyIleLeuPheA 138

199 CTGTATCATCTATCCCTTACTTGGGAATTCCTCTTTGGTTTCTCTGG 248

138 laGly.....LeuGlyGlyTyrPheGlyArgThrPheGluAla 150

249 CTGGAGTTGGAGATCAGTACGACAGCCATATTGGAAAAGGAATTCGCAAA 298

151 IleTyrArgArgTyrLysTyrLysMetSerThrAspMetHisTyrVa 167

299 GTGGAAGATACCTTTATTAGTGAATTTAGT 331

167 lProProGlnLeuGlyLeuIleThrThrValValIleAlaLeuIleProG 184

332 .CAGACCAAGATTCGCATCTCAACAATCATATTTATATATATT...G 377

184 lYlleAlaLeuPheLeuValLeu 191

378 GCTGTGTACTCTTTGTGGCTGTG 400

seq_name: gb_est47:AW644141

seq_documentation_block:

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

US-08-816-011C-2 x AW644141

Align seg 1/1 to: AW644141 from: 1 to: 632

4 AsnArgTrpIleLeuLeuLeuPheThrIleSerTyrLeuMetPheG 20

225 GACCGGGGACCCATCCCTGACATCTGCGTCATCTTCTACCTGTCATGG 274

20 yAlaAlaIleTyrThrHisLeuGluHisGlyGluLeuIleSerArg 37

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/clone_lib="Soares ovary tumor NbHOP"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTCAAGTGGCAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

111 a 83 c 86 g 121 t

alignment_scores:

Quality: 175.50 Length: 141

Ratio: 2.017 Gaps: 5

Percent Similarity: 61.702 Percent Identity: 33.333

alignment_block:

US-08-816-011C-2 x AA464375

Align seg 1/1 to: AA464375 from: 1 to: 401

58 AsnThrThrThrGlnAspGluLeuGlnArgIleSerAspTyrCysAs 74

9 AATTCGACGGAGCTGGATGAAGTCACTCAGCAATATAGTGGCAGCAATAAA 58

74 pLys.....ProValThrLeuProProThrTyrAspThrProT 88

59 TGCAGGGATTATACCGTTAGAAACACCTCCAATCAATCACT 100

88 yrThrThrThrPheThrHisAlaPhePheAlaPheThrValCysSer 104

101 ..CACTGGGATTTGGGAAGTTCCCTCTCTCTGCTGGCACTGTTATTACA 148

105 ThrValGlyTyrGlyAsnIleSerProThrThrPheAlaGlyArgMetII 121

149 ACCATAGATTGGAAACATCTCACACGACACAGCGGCAAAATTT 198

121 eMetIleAlaTyrSerValIleGlyIleProValAsnGlyIleLeuPheA 138

199 CTGTATCATCTATCCCTTACTTGGGAATTCCTCTTTGGTTTCTCTGG 248

138 laGly.....LeuGlyGlyTyrPheGlyArgThrPheGluAla 150

249 CTGGAGTTGGAGATCAGTACGACAGCCATATTGGAAAAGGAATTCGCAAA 298

151 IleTyrArgArgTyrLysTyrLysMetSerThrAspMetHisTyrVa 167

299 GTGGAAGATACCTTTATTAGTGAATTTAGT 331

167 lProProGlnLeuGlyLeuIleThrThrValValIleAlaLeuIleProG 184

332 .CAGACCAAGATTCGCATCTCAACAATCATATTTATATATATT...G 377

184 lYlleAlaLeuPheLeuValLeu 191

378 GCTGTGTACTCTTTGTGGCTGTG 400

seq_name: gb_est47:AW644141

seq_documentation_block:

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

US-08-816-011C-2 x AW644141

Align seg 1/1 to: AW644141 from: 1 to: 632

4 AsnArgTrpIleLeuLeuLeuPheThrIleSerTyrLeuMetPheG 20

225 GACCGGGGACCCATCCCTGACATCTGCGTCATCTTCTACCTGTCATGG 274

20 yAlaAlaIleTyrThrHisLeuGluHisGlyGluLeuIleSerArg 37

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275 GGGCCGCAATATCCAAAGTCTGAGGAGCCCAACTGGAAGCGGCACCTC 324
37 la.....GluGlnArgLysAlaGlnIleAlaIleAsnGlnLysLeuLeu 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 AGCTCTACAAAGGAGAAACAAAGGGAAGATCTGGCCAAAGCAGCTCCTGCCTC 374
52 GluGluLeuGlyAspLysAsnThrThrThrGlnAspGluIleLeuGlnAr 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
375 .....AGCCCCAGGGACCTGGGAAGAATCTGGAGAC 406
68 gIleSerAspTyrCysAspLysProValThrLeuProThrTyrAspA 85
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
407 TGTATCAATGCTGCAGGCAAGGGGTGACCATC.....ACGGGAACA 450
85 spThrProTyrThrThrThrPheTyrHisAlaPhePheAlaPheThr 101
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
451 CTACATTTAACAACTGGAATGGCCCAAGGCTGTATATTTGCTGTACA 500
102 ValCysSerThrValGlyTyrGlyAsnIleSerProThrThrPheAlaG 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
501 GTCATCACCACATAGGCTATGGGAATATGGCCCAAGACACCTGCTGG 550
118 YArgMetIleMetIleAlaTyrSerValIleGlyIleProValAsnGly 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
551 ACGCCTCTTCTGTATATTTACGGCTGTTTGAGTGCCCTCTGCCTGA 600
135 leuPheAlaGlyLeuGlyGluTyrPheGly 145
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
601 CGTGTATCAGCGCCCTGGGAAAGTTTTCGGA 632

```

seq_name: gb_est69:BE309179

seq_documentation_block:

LOCUS BE309179 742 bp mRNA EST 13-JUL-2000
 DEFINITION 601095044F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489466 5',
 mRNA sequence.

ACCESSION BE309179

VERSION BE309179.1 GI:9166970

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 742)

NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

plate: LLAM8530 row: h column: 11

High quality sequence stop: 541.

FEATURES

source

1..742

Location/Qualifiers

/organism="Mus musculus"

/strain="C57/B6"

/db_xref="taxon:10090"

/clone="IMAGE:3489466"

/clone_lib="NCI_CGAP_Mam5"

/tissue_type="tumor, gross tissue"

/dev_stage="7 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;

Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Robin Humphreys,

BASE COUNT 144 a 217 c 202 g 179 t
 ORIGIN

alignment_scores:

Quality: 171.00 Length: 150

Ratio: 1.966 Gaps: 5

Percent Similarity: 58.000 Percent Identity: 31.333

alignment_block:

US-08-816-011c-2 x BE309179

Align seg 1/1 to: BE309179 from: 1 to: 742

```

86 ThrPro.....TyrThrTrpThrPheTyrHisAlaPhePhePheAl 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
12 ACGCCTCGAGGAACATGGAATTCGGACTTCACCTCGCGCTCTCTTCGC 61
99 aPheThrValCysSerThrValGlyTyrGlyAsnIleSerProThrThrP 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 CAGCACCGTGTCTCTCCACACAGGCTATGGCCACACGGTGCCTGTGCAG 111
116 heaLaglyArgMetIleMetIleAlaTyrSerValIleGlyIleProVal 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
112 ATGGGGGCAAGCCTTCTGCATCATCTACTCTGTCATCGCATCCCGTTC 161
133 AsnGlyIleLeuPheAlaGlyLeuGlyGluTyrPheGlyArgThrPheG 149
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
162 ACC....CTCCTCTCTC.....CTGCAC 178
149 uAlaIleTyrArgArgTyrLysLysTyrLysMetSerThrAspMethist 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
179 GGCCTGTGTCACCGTGTACCGTGCATGTCACCCGACAGACAGTCTCT 228
166 yValProProGlnLeuGlyLeu.....IleThrThrValIle 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
229 ACTTCCACATACCTGCGGCTTCTCCAAGCAGGTGGTGGCATGTGCCAT 278
180 AlaLeuIleProGly.....IleAlaLeuPheLeuValLeuProCy 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
279 GCGCTTCTGCTGGGATTTGTCACCGTTTCTCTTCTTCATCCAGC 328
193 sValGlyValHisLeuLeuArgGluLeuGlyLeuSerSerIleSerLeu 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
329 CGCCGTGTTCTCTGTGCTGGAGGATGACTGGAACCTTCTCTCGAGCT 378
210 yTyrSerTyrValThrThrThrThrIleGlyPheGlyAspTyrValPro 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
379 ACTTCTGTTTCTATCTCTCCCTGAGCACCATCGGCTGGGGGACTATGTCCA 428

```

seq_name: gb_est27:AI956401

seq_documentation_block:

LOCUS AI956401 676 bp mRNA EST 20-AUG-1999

DEFINITION ul74g11.y1 Sugano mouse kidney mkia Mus musculus cDNA clone

IMAGE:2136356 5' similar to TR:000180 O00180 POTASSIUM CHANNEL

KCNOL1.; mRNA sequence.

ACCESSION AI956401

VERSION AI956401.1 GI:5749110

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 676)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person

,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter

,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

JOURNAL

COMMENT

Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1001032

Possible reversed clone: similarity on wrong strand

Seq primer: custom primer used

High quality sequence stop: 519.

Location/Qualifiers

FEATURES

source

```
1. .676
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone_lib="IMAGE:2136356"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGG); Site_2: DraIII (CACCATGG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGG, 3' site CACCATGG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGGTGG and 3' end
primer CCACCTGCAGCTCGACACA."
```

BASE COUNT 94 a 216 c 211 g 153 t 2 others
ORIGIN

alignment_scores:

Quality: 170.00 Length: 190
Ratio: 1.604 Gaps: 6
Percent Similarity: 55.789 Percent Identity: 27.895

alignment_block:

US-08-816-011c-2 x AI956401 ..

Align seg 1/1 to: AI956401 from: 1 to: 676

```
9 LeuLeuIlePheTyrIleSerTyrLeuMetPheGlyAlaAlaIleTyrTy 25
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
131 CTGGTGTGGGCTACCTCTACTGCTGTGTCGGCGCGGTCTTCTC 180

25 rHisIleGluHisGlyGluGluLysIleSerArgAlaGluGlnArgLysA 42
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 GTCCGTGGAGCTGCTTATGAGGACCTGCTGCCGAGGAGCTGGCAAG. 229

42 LaGlnIleAlaIleAsnGlnTyrIleLeuGluLeuGlyAspLysAsn 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
230 .....CTGAAGCGCGCTTCTTGGAGGAGCAGGAGTGCCTGTCG 268

59 ThrThrThrGlnAspGluIleGlnArgIleSerAspTyrCysAspLy 75
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
269 GAGCGGAGCTGGAGAGCTTCTTGGCGCGCTGCTGGAGGCCAGCAATTA 318

75 sproValThrLeuProThrThrThrAspThrProThrThrThrThr 92
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
319 TGGAGTGTGCTGCTCAGCAACGCTCGGAAAT...TGGAAATGGGACT 365

92 heTyrHisAlaPhePhePheAlaPheThrValCysSerThrValGlyTyr 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
366 TCACCTGGCGCTCTTCTTCCACGACCGCTCTCCACCAAGGCTAT 415
```

```
109 GlyAsnIleSerProThrThrPheAlaGlyArgMetIleMetIleAlaTy 125
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
416 GGCCACACGGTGGCCCTCTCAGATGGGGGCAAGCCTTCTGCATCATCTA 465

125 rSerValIleGlyIleProValAsnGlyIleLeuPheAlaGlyLeuGlyG 142
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
466 CTCTGTCTATCGGCATCCCGTTTCAAC...CTCCTCTTC..... 499

142 LuTyrPheGlyArgThrPheGluAlaIleTyrArgArgTyrLysLysTyr 158
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
500 .....CTGACGGCGCTGGTCCACGCTGTCACCGTGCAT 532

159 LysMetSerThrAspMetHisTyrValProGlnLeuGlyLeu..... 173
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
533 GTCACCCCGCAGACCATCTCTACTTCCACATACGCTGNGGCTTCTCCAA 582

174 ....IleThrThrValIleAlaLeuIleProGly.....IleA 186
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
583 GCAGGTGGTGGCATTTGCCATGCGGTTCTGCTGCTGCTGCTGCTGCTG 632

186 laLeuPheLeuValLeuPro 192
|||||:|||||:|||||:|||||:|||||:|||||:
633 CTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT
```